

SEQUENCE LISTING

<110> Benjanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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<141> 2001-11-13

<150> US 09/924,340
<151> 2001-08-06

<150> PCT/IB01/01715
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<150> US 60/305,456
<151> 2001-07-13

<150> US 60/302,277
<151> 2001-06-29

<150> US 60/298,698
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<150> US 60/293,574
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Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
20 25 30
gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581
Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
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atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629
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50 55 60 65
gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677
Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
70 75 80
aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac 1725
Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
85 90 95
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Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile
100 105 110
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Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
115 120 125
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Gln Lys Gly Lys Lys
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ggc	act	ggg	ttc	agt	tat	gtg	aat	ggg	agt	ggg	gcc	tat	gcc	aag	gac	440
Gly	Thr	Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	
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ctg	gct	atg	gtg	gct	tca	gac	atg	atg	gtt	ctc	ctg	aag	acc	ttc	ttc	488
Leu	Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	
		110			115					120					125	
agt	tgc	cac	aaa	gaa	ttc	cag	aca	gtt	cca	ttc	tac	att	ttc	tca	gag	536
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	Glu	
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Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	Tyr	Lys	
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gcc	att	cag	cga	ggg	acc	atc	aag	tgc	aac	ttt	gcg	ggg	gtt	gcc	ttg	632
Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	Val	Ala	Leu	
		160					165						170			
ggg	gat	tcc	tgg	atc	tcc	cct	gtt	gat	tcg	gtg	ctc	tcc	tgg	gga	cct	680
Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	Ser	Trp	Gly	Pro	
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Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	Gly	Leu	Ala	Glu	Val	
		190			195					200					205	
tct	aag	gtt	gca	gag	caa	gta	ctg	aat	gcc	gta	aat	aag	ggg	ctc	tac	776
Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	Val	Asn	Lys	Gly	Leu	Tyr	
			210						215					220		
aga	gag	gcc	aca	gag	ctg	tgg	ggg	aaa	gca	gaa	atg	atc	att	gaa	cag	824
Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	Ala	Glu	Met	Ile	Ile	Glu	Gln	
			225					230					235			
gta	aaa	agg	gga	aac	act	cag	agg	cta	gcc	tgc	ttg	gct	ttt	tct	ggg	872
Val	Lys	Arg	Gly	Asn	Thr	Gln	Arg	Leu	Ala	Cys	Leu	Ala	Phe	Ser	Gly	
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ggg	tac	agg	gcc	cat	ggg	tgg	tgt	tgt	caa	act	tgg	agt	cta	cac		917
Gly	Tyr	Arg	Ala	His	Gly	Trp	Cys	Cys	Gln	Thr	Trp	Ser	Leu	His		
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 -10 -5 1 5
 Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
 10 15 20
 Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn
 25 30 35
 Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly
 40 45 50
 Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
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1000

[illegible]

1

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Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
          45          50          55
tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357
Ser Ile Val Thr
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taaataaaaa aaaaaaaaaa a 438

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Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
          15          20          25
Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
30          35          40          45
Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr
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Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val

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5      10      15      20
tcc atc tcc tgc agg tct agt cag agc ctc ctg cat gtt caa ggg tcc 196
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Val Gln Gly Ser
25      30      35
aac tat ttg gat tgg tac cac cag aag cca ggg cag tct cca caa ctc 244
Asn Tyr Leu Asp Trp Tyr His Gln Lys Pro Gly Gln Ser Pro Gln Leu
40      45      50
ctg ata tac ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 292
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
55      60      65
agt ggc agt gga tca ggc aca gat ttc aca ctg aaa atc agt aga gtg 340
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
70      75      80
gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct cta caa act 388
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
85      90      95      100
cca ttc act ttc ggc cct ggg acc aga gtg gat atc aag cga act gtg 436
Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
105      110      115
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 484
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
120      125      130
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Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
135      140      145
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 580
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
150      155      160
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 628
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165      170      175      180
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 676
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
185      190      195
gtc tac gcc tgc gaa gtc acc cat cag gcc ctg agc tcg ccc gtc aca 724
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
200      205      210
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Lys Ser Phe Asn Arg Gly Glu Cys
215      220
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cccctattgc ggtcctccag ctcatctttc acctcacccc cctcctcctc cttggcttta 898
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 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser

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 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
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 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
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 gccctcagge ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccctt 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
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 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15

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Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
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ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35      40      45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50      55      60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
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agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80      85      90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
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      20      25      30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35      40      45      50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55      60      65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
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Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
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gcctcaggc ctcaggcctt ccttggttg aagattgggc ttcacctggg acctaccct 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala

-10 -5
aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
1 5 10 15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
20 25 30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
35 40 45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
50 55 60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Cys Gln Asp Asn Ser Asp Glu Glu
65 70 75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80 85 90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
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Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
5 10 15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
20 25 30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35 40 45 50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
55 60 65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
70 75 80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
85 90

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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
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 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
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 20 25 30
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 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
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 aaccctctcg agcaagacgt ggtgatgcca attggtggaa aggagaaaat cacagaggaa 180
 taggactttt cccatccaat tttgtaacaa ctaatttaaa catagagact gaggcagcgg 240
 ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300
 agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353
 Met Asp Arg Ala Leu Gln Val Leu Gln
 1 5
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 Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
 10 15 20 25
 tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt 449
 Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
 30 35 40
 gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa 497
 Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
 45 50 55
 gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545
 Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
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 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
 75 80 85
 gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641
 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
 90 95 100 105
 gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
 Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
 110 115 120
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 Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
 125 130 135
 aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785
 Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
 140 145 150
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 Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
 155 160 165

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Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met
170                      175                      180                      185
ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg      929
Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
                      190                      195                      200
cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca      977
Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
                205                      210                      215
cag cag cac aca aat tac cat cag cag cct ctc ctt tagaaacaaa      1023
Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
                220                      225
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<211> 229

<212> PRT

<213> Homo sapiens

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Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
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Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
                50                      55                      60
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
65                      70                      75                      80
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
                85                      90                      95
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
                100                      105                      110
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
                115                      120                      125
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
                130                      135                      140
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
145                      150                      155                      160
Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
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Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
                180                      185                      190
Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
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Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
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Gln Gln Pro Leu Leu
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                                         Met Arg
                                         -15
gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165
Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
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cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213
Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
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gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261
Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val
                        20                        25                        30
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Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val
35                        40                        45                        50
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Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
                        55                        60                        65
tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405
Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
                        70                        75                        80
acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453
Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
                        85                        90                        95
gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501
Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
100                        105                        110
acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549
Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
115                        120                        125                        130
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Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
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ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645
Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
                        150                        155                        160
tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg 693
Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
                        165                        170                        175
cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741
Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
180                        185                        190
cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789
His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
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Lys Ala Lys Ile Lys Ser Glu Met
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                                         844

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 20 25 30
 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
 35 40 45
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
 50 55 60
 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
 65 70 75
 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
 80 85 90 95
 Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
 100 105 110
 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
 115 120 125
 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
 130 135 140
 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
 145 150 155
 Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
 160 165 170 175
 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
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 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val
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 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
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Tyr	Asp	Tyr	Gly	Thr	Asp	Asn	Phe	Glu	Glu	Ser	Ile	Phe	Ser	Gln	Asp	
15							20				25					
tat	gag	gat	aaa	tac	ctg	gat	gga	aaa	aat	att	aag	gaa	aaa	gaa	act	312
Tyr	Glu	Asp	Lys	Tyr	Leu	Asp	Gly	Lys	Asn	Ile	Lys	Glu	Lys	Glu	Thr	
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gtg	ata	ata	ccc	aat	gag	aaa	agt	ctt	caa	tta	caa	aaa	gat	gag	gca	360
Val	Ile	Ile	Pro	Asn	Glu	Lys	Ser	Leu	Gln	Leu	Gln	Lys	Asp	Glu	Ala	
45					50					55					60	
ata	aca	cca	tta	cct	ccc	aag	aaa	gaa	aat	gat	gaa	atg	ccc	acg	tgt	408
Ile	Thr	Pro	Leu	Pro	Pro	Lys	Lys	Glu	Asn	Asp	Glu	Met	Pro	Thr	Cys	
				65				70					75			
ctg	ctg	tgt	gtt	tgt	tta	agt	ggc	tct	gta	tac	tgt	gaa	gaa	gtt	gac	456
Leu	Leu	Cys	Val	Cys	Leu	Ser	Gly	Ser	Val	Tyr	Cys	Glu	Glu	Val	Asp	
		80					85				90					
att	gat	gct	gta	cca	ccc	tta	cca	aag	gaa	tca	gcc	tat	ctt	tac	gca	504
Ile	Asp	Ala	Val	Pro	Pro	Leu	Pro	Lys	Glu	Ser	Ala	Tyr	Leu	Tyr	Ala	
	95					100					105					
cga	ttc	aac	aaa	att	aaa	aag	ctg	act	gcc	aaa	gat	ttt	gca	gac	ata	552
Arg	Phe	Asn	Lys	Ile	Lys	Lys	Leu	Thr	Ala	Lys	Asp	Phe	Ala	Asp	Ile	
	110				115				120							
cct	aac	tta	aga	aga	ctc	gat	ttt	aca	gga	aat	ttg	ata	gaa	gat	ata	600
Pro	Asn	Leu	Arg	Arg	Leu	Asp	Phe	Thr	Gly	Asn	Leu	Ile	Glu	Asp	Ile	
125				130				135							140	
gaa	gat	ggg	act	ttt	tca	aaa	ctt	tct	ctg	tta	gaa	gaa	ctt	tca	ctt	648
Glu	Asp	Gly	Thr	Phe	Ser	Lys	Leu	Ser	Leu	Leu	Glu	Glu	Leu	Ser	Leu	
			145					150					155			
gct	gaa	aat	caa	cta	cta	aaa	ctt	cca	gtt	ctt	cct	ccc	aag	ctc	act	696
Ala	Glu	Asn	Gln	Leu	Leu	Lys	Leu	Pro	Val	Leu	Pro	Pro	Lys	Leu	Thr	
		160				165					170					
tta	ttt	aat	gca	aaa	tac	aac	aaa	atc	aag	agt	agg	gga	atc	aaa	gca	744
Leu	Phe	Asn	Ala	Lys	Tyr	Asn	Lys	Ile	Lys	Ser	Arg	Gly	Ile	Lys	Ala	
	175					180					185					
aat	gca	ttc	aaa	aaa	ctg	aat	aac	ctc	acc	ttc	ctc	tac	ttg	gac	cat	792
Asn	Ala	Phe	Lys	Lys	Leu	Asn	Asn	Leu	Thr	Phe	Leu	Tyr	Leu	Asp	His	
	190				195					200						
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Asn	Ala	Leu	Glu	Ser	Val	Pro	Leu	Asn	Leu	Pro	Glu	Ser	Leu	Arg	Val	
205				210				215							220	
att	cat	ctt	cag	ttc	aac	aac	ata	gct	tca	att	aca	gat	gac	aca	ttc	888
Ile	His	Leu	Gln	Phe	Asn	Asn										

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aaatgagaat ctcacataa aattagttca agcataagat gaaaacagaa tattctgtgg 1930
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<210> 22
<211> 298
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<213> Homo sapiens

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Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
30 35 40 45
Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr
50 55 60
Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu
65 70 75
Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp
80 85 90
Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe
95 100 105
Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn
110 115 120 125
Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp
130 135 140
Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu
145 150 155
Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe
160 165 170
Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala
175 180 185
Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala
190 195 200 205
Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His
210 215 220
Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys
225 230 235
Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu
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<210> 23
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Variable	Mean	SD	Min	Max
Age	35.2	10.5	20	55
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	1.5	9	16
Income	3500	1500	1000	7000
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	15.0	55	85
Work-life balance	65.0	18.0	45	85
Family support	75.0	20.0	55	95
Community involvement	60.0	25.0	35	85
Personal growth	65.0	22.0	40	90
Overall well-being	70.0	18.0	50	90

Variable	Mean	SD	Min	Max
Age	35.2	10.5	20	55
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	1.5	9	16
Income	3500	1500	1000	7000
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	15.0	55	85
Work-life balance	65.0	18.0	45	85
Family support	75.0	20.0	55	95
Community involvement	60.0	25.0	35	85
Personal growth	65.0	22.0	40	90
Overall well-being	70.0	18.0	50	90

Variable	Mean	SD	Min	Max
Age	35.2	10.5	20	55
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	1.5	9	16
Income	3500	1500	1000	7000
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	15.0	55	85
Work-life balance	65.0	18.0	45	85
Family support	75.0	20.0	55	95
Community involvement	60.0	25.0	35	85
Personal growth	65.0	22.0	40	90
Overall well-being	70.0	18.0	50	90

Variable	Mean	SD	Min	Max
Age	35.2	10.5	20	55
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	1.5	9	16
Income	3500	1500	1000	7000
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	15.0	55	85
Work-life balance	65.0	18.0	45	85
Family support	75.0	20.0	55	95
Community involvement	60.0	25.0	35	85
Personal growth	65.0	22.0	40	90
Overall well-being	70.0	18.0	50	90

Variable	Mean	SD	Min	Max
Age	35.2	10.5	20	55
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	1.5	9	16
Income	3500	1500	1000	7000
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	15.0	55	85
Work-life balance	65.0	18.0	45	85
Family support	75.0	20.0	55	95
Community involvement	60.0	25.0	35	85
Personal growth	65.0	22.0	40	90
Overall well-being	70.0	18.0	50	90

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cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
      240                245                250
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca 867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
      255                260                265                270
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc 915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
      275                280                285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc 963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
      290                295                300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc cct 1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
      305                310                315
ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca 1059
Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
      320                325                330
gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc 1107
Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
      335                340                345                350
gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc 1155
Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
      355                360                365
ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc 1203
Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Ile Ser
      370                375                380
ctg ctg aag tgaggaggcc catgggcaga agatagggat tcccctggac 1252
Leu Leu Lys
      385
cacacctccg tgggttcactt tggtcacaag taggagacac agatggcacc tgtggccaga 1312
gcacctcagg accctcccca cccaccaaata gcctctgcct tgatggagaa ggaaaaggct 1372
ggcaagggtgg gttccaggga ctgtacctgt aggagacaga aaagagaaga aagaagcact 1432
ctgctggcgg gaatactctt ggtcacctca aatttaagtc gggaaattct gctgcttgaa 1492
acttcagccc tgaacctttg tcaccattcc tttaaattct ccaaccctaa gtattcttct 1552
tttcttagtt tcagaagtac tggcatcaca cgcaaggttac cttggcgtgt gtccctgtgg 1612
taccctggca gagaagagac caagcttggtt tccttgctgg ccaaagtcag taggagagga 1672
tgcacagttt gctattttgct ttagagacag ggactgtata aacaagccta acattggtgc 1732
aaaaaaaaaa aaaa 1746

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<210> 24
<211> 401
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..17

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<400> 24
Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly
      -15                -10                -5
Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
      1                5                10                15
Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
      20                25                30
Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
      35                40                45
Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
      50                55                60

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Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Pro	Glu	Pro
65						70					75				
Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser
80					85					90					95
Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu
				100						105				110	
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu
			115						120				125		
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr
		130					135					140			
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met
		145				150					155				
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr
160					165					170					175
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser
				180						185				190	
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu
			195					200					205		
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile
		210					215					220			
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser
		225				230					235				
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp
240					245					250					255
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser
				260					265					270	
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val
			275					280					285		
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys
		290					295					300			
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val
		305				310					315				
Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu
320					325					330					335
Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu
				340					345					350	
Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg
			355					360				365			
Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser	Leu	Leu
		370					375					380			

Lys

<210> 25
 <211> 1239
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..126

<220>
 <221> CDS
 <222> 127..879

<220>
 <221> 3'UTR
 <222> 880..1239

<220>
 <221> polyA_site
 <222> 1224..1239

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<400> 25
agtctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg 60
gccaggagag tccccacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag 120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
            -20                    -15                    -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
            -5                    1                    5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca 264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
            10                    15                    20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat 312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
            25                    30                    35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
            40                    45                    50                    55
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
            60                    65                    70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
            75                    80                    85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc 504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
            90                    95                    100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
            105                    110                    115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
            120                    125                    130                    135
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
            140                    145                    150
cgg cgg cac acc cgg agc gcc gag gac gac tgc gag cgg gac ccc ctg 696
Arg Arg His Thr Arg Ser Ala Glu Asp Ser Glu Arg Asp Pro Leu
            155                    160                    165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt 744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
            170                    175                    180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac 792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
            185                    190                    195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga 840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
            200                    205                    210                    215
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgt 889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
            220                    225
ggaagggcac cctctttaac ccatecctca gcaaacgcag ctcttcccaa ggaccaggtc 949
ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct 1009
ggggtccctt ccacaggagg tctgtgaga accaaccttt gaggcccaag tcatgggggtt 1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaaa 1129
ctagaaattt ccccttcatg aaggtagaga gaaggggtct ctcccaacat atttctcttc 1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa 1239

<210> 26
<211> 251
<212> PRT
<213> Homo sapiens

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<220>
 <221> SIGNAL
 <222> 1..24

<400> 26
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 -20 -15 -10
 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225

<210> 27
 <211> 1179
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..115

<220>
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 <222> 116..961

<220>
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 <222> 962..1179

<220>
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 <222> 1145..1150

<220>
 <221> polyA_site
 <222> 1164..1179

<400> 27

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acaaattccc aatgcagtta caggatcctg ggaagcagag tgtctggatg gaacctgagc 60
tgggtctctg actcacttct gacttttaggc gctcgaggac tgtgcccagg agcag atg 118
                                         Met
                                         1
cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166
Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln
                    5                    10                    15
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt 214
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu
                    20                    25                    30
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln
                    35                    40                    45
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly
                    50                    55                    60                    65
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr
                    70                    75                    80
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct 406
Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser
                    85                    90                    95
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly
                    100                    105                    110
ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa 502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys
                    115                    120                    125
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac 550
Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp
                    130                    135                    140                    145
ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc 598
Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe
                    150                    155                    160
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat 646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr
                    165                    170                    175
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg 694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val
                    180                    185                    190
cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga 742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg
                    195                    200                    205
gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc 790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly
                    210                    215                    220                    225
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac 838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr
                    230                    235                    240
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc 886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr
                    245                    250                    255
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg 934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg
                    260                    265                    270
cca aat gat ttt att cca aat gta att taattgctgc tgttgggctt 981
Pro Asn Asp Phe Ile Pro Asn Val Ile
                    275                    280
tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatatc 1041
catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt 1101
tacttaaatgt gctttcagta cagcagatat gcaatattca ccaataaataa gtagactgtg 1161
tcaaaaaaaaa aaaaaaaaaa
                                         1179

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<210> 28
 <211> 282
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

<400> 28
 Met Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln
 1 5 10 15
 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
 20 25 30
 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
 85 90 95
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
 100 105 110
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
 115 120 125
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
 130 135 140
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
 145 150 155 160
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
 165 170 175
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 180 185 190
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 195 200 205
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 210 215 220
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 225 230 235 240
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 245 250 255
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 260 265 270
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280

<210> 29
 <211> 1118
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..344

<220>
 <221> CDS
 <222> 345..1118

<220>
 <221> polyA_site
 <222> 1103..1118

<400> 29

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tgtggcctgg ggaaggagg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120
tggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtc 180
aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
cgccccgcag tagctgcaga ctccgccgc gacgtgtgcg cgcttctctg ggccagagcg 300
agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
                                     Met Gly Arg Thr
cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
-15 -10 -5 1
tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
5 10 15
atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
20 25 30
gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
35 40 45
aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
50 55 60 65
gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
70 75 80
gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
85 90 95
gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
100 105 110
tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
115 120 125
ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
130 135 140 145
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
150 155 160
cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
165 170 175
aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
180 185 190
atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
195 200 205
act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
210 215 220 225
gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa 1118
Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys

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<210> 30
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>
 <221> UNSURE
 <222> 49
 <223> Xaa = Glu, *

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 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp
 1 5 10
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
 15 20 25
 Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
 30 35 40
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
 45 50 55 60
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
 65 70 75
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
 80 85 90
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
 95 100 105
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
 110 115 120
 Pro Gly Gly Arg Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
 125 130 135 140
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
 145 150 155
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
 160 165 170
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
 175 180 185
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
 190 195 200
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
 205 210 215 220
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
 225 230 235
 Lys Lys

<210> 31
 <211> 1273
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..13

<220>
 <221> CDS
 <222> 14..1048

<220>
 <221> 3'UTR
 <222> 1049..1273

<220>
 <221> polyA_signal
 <222> 1234..1239

<220>
 <221> polyA_site
 <222> 1258..1273

<400> 31

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agagggttggg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc      49
          Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
          -25                      -20                      -15
tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
          -10                      -5                      1
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac      145
Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
          5                      10                      15
ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt      193
Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val
          20                      25                      30                      35
gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga      241
Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg
          40                      45                      50
agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc      289
Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro
          55                      60                      65
tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt      337
Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe
          70                      75                      80
aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg      385
Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu
          85                      90                      95
aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg      433
Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu
          100                      105                      110                      115
gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac      481
Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn
          120                      125                      130
aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att      529
Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
          135                      140                      145
ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg      577
Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
          150                      155                      160
cag cgg aca atg atc aga tat ttc aca tgc aat cca gcc tca aag gtc      625
Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
          165                      170                      175
ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt      673
Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
          180                      185                      190                      195
cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata      721
His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile
          200                      205                      210
gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca      769
Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala
          215                      220                      225
ggg gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga      817

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Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly		
	230						235					240					
aga	tat	gga	cca	tca	ctt	ggt	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865	
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met		
	245						250				255						
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913	
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala		
	260					265				270					275		
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggt	cat	961	
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His		
				280					285					290			
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa	1009	
Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu		
			295					300					305				
ata	agg	act	aat	ggc	ccc	aaa	aaa	gga	ggt	ggc	tct	aag	taaaactggg			1058	
Ile	Arg	Thr	Asn	Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys					
	310					315					320						
attggacagt	agtgggtgcat	ctgggtccttg	ccgcctgaga	gccccaggag	acatcggtcta	1118											
gagtgaccat	ggctatgctc	ccgtctggaa	gatgccagca	tctggcctcc	cacttttttc	1178											
agctgtgtcc	cccagtcctg	gtcttttttag	aatgtgaatg	atgataaagt	tgtgaaataa	1238											
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 <213> Homo sapiens

<220>
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Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	Leu	Thr	Ala	Val		
	-10				-5					1				5			
Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	Phe	Phe	Ile	Gln		
		10						15					20				
Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	Glu	Pro	Arg	Arg		
		25					30					35					
Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	Ser	Ala	Leu	Ile		
	40					45					50						
Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	Tyr	Pro	Ile	Arg		
	55					60				65				70			
Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	Thr	Gly	Cys	Ala		
			75						80					85			
Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	Lys	Ser	Arg	Val		
		90						95					100				
Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	Asp	Ser	Ile	Arg		
	105					110						115					
Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	Lys	Trp	Trp	Asn		
	120					125						130					
Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	Ile	Ala	Ala	Asn		
	135				140					145					150		
Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	Gln	Arg	Thr	Met		
			155					160						165			
Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	Leu	Cys	Ser	Pro		
		170						175					180				
Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	His	Met	Ala	Ala		
	185						190					195					
Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	Val	Asn	Ile	Leu		
	200					205					210						
Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	Gly	Val	Ile	Ser		

215 220 225 230
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 235 240 245
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 250 255 260
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 265 270 275
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Ser Lys
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 <213> Homo sapiens

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 <222> 73..672

<220>
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<220>
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 <222> 708..723

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 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447

Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
 110 115 120 125
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
 130 135 140
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
 Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
 145 150 155
 gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
 Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
 160 165 170
 agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
 Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
 175 180 185
 cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
 His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
 190 195 200
 aagatgtgtt aaaataaaaa aaaaaaaaaa t 723

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 <211> 200
 <212> PRT
 <213> Homo sapiens

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 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 35 40 45
 Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
 50 55 60
 Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
 65 70 75 80
 Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
 85 90 95
 Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
 100 105 110
 Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
 115 120 125
 Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
 130 135 140
 Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
 145 150 155 160
 Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
 165 170 175
 Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
 180 185 190
 Asp Cys Asp Cys Glu Gln Cys Cys
 195 200

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 <212> DNA
 <213> Homo sapiens

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<222> 119..655

<220>

<221> 3'UTR

<222> 656..845

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<221> polyA_signal

<222> 809..814

<220>

<221> polyA_site

<222> 830..845

<400> 35

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taaattctgc caaaaggact gaggaacggg gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggg 755
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cagtttatta tcgcaaaaaa aaaaaaaaaa 845
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<210> 36

<211> 179

<212> PRT

<213> Homo sapiens

<400> 36

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 20 25 30
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
 100 105 110
 Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
 115 120 125
 Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
 130 135 140
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 145 150 155 160
 Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
 165 170 175

Gly Pro Tyr

<210> 37
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 <212> DNA
 <213> Homo sapiens

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<220>
 <221> CDS
 <222> 17..259

<220>
 <221> 3'UTR
 <222> 260..517

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 Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
 15 20 25
 gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
 Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
 30 35 40
 gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
 Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
 45 50 55 60
 aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
 Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
 65 70 75
 gga caa gaa ata gcc tgaccatgag gaccagggag ctgctacccc tccctacagc 299
 Gly Gln Glu Ile Ala
 80
 tcctaccctc tggctgcaat ggggctgcac tgtgagccct gcccacaaca gatgcatcct 359
 gctctgacag gtgggtcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419
 tttctccaat ggacatgatt cccaagtcatt cctgctgcct tttttcttat agacacaatg 479
 aacagaccac ccacaacctt agttctctaa gtcacatcct 517

<210> 38
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 38
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 20 25 30
 Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
 35 40 45
 Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
 50 55 60
 Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
 65 70 75 80
 Ala

<210> 39
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 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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<220>
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<220>
 <221> polyA_site
 <222> 1801..1816

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 gcctcacttc gtcccactgt ggtaggggt gagtcttgcg aatgttaagt gatttgctca 180
 aggtgcccac ttcgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
 -15 -10
 ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
 -5 1 5
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
 10 15 20
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
 25 30 35 40
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tgc tgg gtg ggg ccc 484
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro

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      45      50      55
aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
      60      65      70
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His
      75      80      85
gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc 628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
      90      95      100
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc 676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
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ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc 724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
      125      130      135
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc 772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
      140      145      150
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Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr
      155      160      165
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc 868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
      170      175      180
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg 916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu
      185      190      195      200
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag 964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
      205      210      215
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac 1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
      220      225      230
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgctc 1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
      235      240
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gaccgtcttg actggctgga gccttcaaag ccactgggat gtcctccagg cacctgggtc 1718
ccatgaccag ctccccgtct ccataggggt aggcatttca ctggtttatg aagctcgagt 1778
ttcattaaat atgttaagaa tcaaaaaaaaa aaaaaaaaa 1816

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<210> 40

<211> 263

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..20

<400> 40

Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu Leu Leu Gly Ser Leu

-20

-15

-10

-5


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Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
-20 -15 -10
gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
-5 1 5 10
gct gac cag aac tgc acg caa gag tgc gtc tgc gac agc gaa tgc gcc 258
Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
15 20 25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
30 35 40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
45 50 55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
60 65 70 75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
80 85 90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
95
agtttctgcc tggccctgca tctggttcca gccacactgc cctccccctt ttcgggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaa aaaaaaaaaa a 643

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<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..30

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<400> 42
Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser
-30 -25 -20 -15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
-10 -5 1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
5 10 15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
20 25 30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
35 40 45 50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
55 60 65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
70 75 80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
85 90

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<210> 43
<211> 501
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..227

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<220>
 <221> CDS
 <222> 228..501

<400> 43
 actcttactc tttctctctc actctctctc ttttcccacc ctttaagccaa gtacagggat 60
 agttgtctca tcattgggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
 ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
 ccattggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
 Met Gln Gly
 -30
 act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
 Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
 -25 -20 -15
 aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
 Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
 -10 -5 1
 aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
 Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
 5 10 15
 cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
 Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
 20 25 30 35
 gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
 Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
 40 45 50
 gtt cct ttc tcc gaa ctg aaa gac a 501
 Val Pro Phe Ser Glu Leu Lys Asp
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<210> 44
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..33

<400> 44
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 -30 -25 -20
 Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Leu
 -15 -10 -5
 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
 1 5 10 15
 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
 20 25 30
 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
 35 40 45
 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
 50 55

<210> 45
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
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 <221> CDS
 <222> 98..934

<220>
 <221> 3'UTR
 <222> 935..960

<400> 45

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ataatcacct ctcattccag actatgtag gtcttaatgg tgggaggacg cccgagtgc 60
cggcccgttt caccgcagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
                                Met Thr Pro Ser Glu Gly
                                1           5
gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
                                10           15           20
gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
                                25           30           35
cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259
Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
                                40           45           50
caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
                                55           60           65           70
ggg ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
                                75           80           85
aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
                                90           95           100
ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
                                105           110           115
gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Arg Leu Pro
                                120           125           130
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
                                135           140           145           150
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
                                155           160           165
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
                                170           175           180
ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
                                185           190           195
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr
                                200           205           210
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly
                                215           220           225           230
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta 835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val
                                235           240           245
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt 883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly
                                250           255           260
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga 931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly

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265 270 275 960
 ttc tagggatggg gcagagtggc agcatc
 Phe

<210> 46
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu
 1 5 10 15
 Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val Leu Leu Arg Asp
 20 25 30
 Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
 35 40 45
 Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
 50 55 60
 Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
 65 70 75 80
 Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
 85 90 95
 Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
 100 105 110
 Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
 115 120 125
 Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
 130 135 140
 Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Val Gly Lys
 145 150 155 160
 Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
 165 170 175
 Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
 180 185 190
 Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
 195 200 205
 Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
 210 215 220
 Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
 225 230 235 240
 Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
 245 250 255
 Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
 260 265 270
 Trp Gly Trp Gly Gln Gly Phe
 275

<210> 47
 <211> 1294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..266

<220>
 <221> CDS
 <222> 267..1139

<220>
 <221> 3'UTR
 <222> 1140..1294

<220>
 <221> polyA_signal
 <222> 1246..1251

<220>
 <221> polyA_site
 <222> 1279..1294

<400> 47
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 aaattcttac ctgcgtcttt cactgctagt aagatcagat tgcgtttctt tcagttactc 120
 ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
 ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
 gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
 Met Ile Tyr Thr Met Lys Lys Val His
 -25 -20
 gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
 Ala Leu Trp Ala Ser Val Cys Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25 30
 gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
 Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 35 40 45
 att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
 Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
 80 85 90
 cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
 Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
 95 100 105 110
 gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
 Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
 115 120 125
 aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
 Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
 130 135 140
 cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821
 Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
 145 150 155
 act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869
 Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
 160 165 170
 tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917
 Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
 175 180 185 190
 aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
 Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
 195 200 205
 tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013
 Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
 210 215 220
 tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061

Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
 225 230 235
 ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109
 Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile
 240 245 250
 gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159
 Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
 255 260
 aacattaatt ctactaaata ttttatatga aatgtttcac tatgattttc tatttttctt 1219
 ctaaaatgct ttttaattaat atgttcatta aattttctat gcttattgta cttgtttacca 1279
 aaaaaaaaaa aaaaaa 1294

<210> 48
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400> 48
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 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
 40 45 50
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
 55 60 65
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
 70 75 80
 Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
 85 90 95 100
 Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
 105 110 115
 Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
 120 125 130
 Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
 135 140 145
 Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
 150 155 160
 Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
 165 170 175 180
 Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
 185 190 195
 Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
 200 205 210
 Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
 215 220 225
 Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
 230 235 240
 Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
 245 250 255 260
 Lys Asn Met

<210> 49
 <211> 1194
 <212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..47

<220>

<221> CDS

<222> 48..1100

<220>

<221> 3'UTR

<222> 1101..1194

<220>

<221> polyA_signal

<222> 1159..1164

<220>

<221> polyA_site

<222> 1179..1194

<400> 49

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ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct      56
                                     Met Pro Ser
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc      104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20                               -15          -10          -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag      152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
                               1           5           10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa      200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
                               15          20          25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc      248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
                               30          35          40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta      296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
                               45          50          55          60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc      344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
                               65          70          75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac      392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
                               80          85          90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag      440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
                               95          100         105
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt      488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
                               110         115         120
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag      536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
                               125         130         135         140
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag      584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
                               145         150         155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg      632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
                               160         165         170
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg      680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
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      175      180      185
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
      190      195      200
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu
205      210      215      220
cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc 824
His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val
      225      230      235
ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc 872
Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu
      240      245      250
tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat 920
Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His
      255      260      265
aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc 968
Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
      270      275      280
atg ttt tta gag gcc ata ccc atg tct atc ccc gag gtc aag ttc 1016
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe
285      290      295      300
aac aaa ccc ttt gtc ttc tta atg att gac caa aat acc aag tct ccc 1064
Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro
      305      310      315
ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa taactgcctc 1110
Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys
      320      325
tcgctcctca acccctcccc tccatccctg gccccctccc tggatgacat taaagaaggg 1170
ttgagctgaa aaaaaaaaaa aaaa 1194

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<210> 50
<211> 351
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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Cys Leu Val Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
      -5      1      5
Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
10      15      20
Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
25      30      35      40
Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
      45      50      55
Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
      60      65      70
Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
      75      80      85
Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
90      95      100
Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
105      110      115      120
Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
      125      130      135
Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro
140      145      150

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Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys	Lys	Lys	Leu
		155					160					165			
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala	Ile
		170				175					180				
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu	Leu
185					190					195					200
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser
			205						210					215	
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu
			220					225						230	
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly
		235					240					245			
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys
	250					255					260				
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala
265					270					275					280
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu
			285						290					295	
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn	Thr
			300					305					310		
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys	
		315					320						325		

<210> 51
 <211> 1317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..289

<220>
 <221> CDS
 <222> 290..1162

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 <221> 3'UTR
 <222> 1163..1317

<220>
 <221> polyA_signal
 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1302..1317

<400> 51
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 cgactttagg ctggataata gtcaaattct tacctcgctc tttcactgct agtaagatca 120
 gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180
 aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact 240
 ccgttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac 298
 Met Ile Tyr
 -25
 aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346
 Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu
 -20 -15 -10
 aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa 394
 Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu
 -5 1 5
 cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat 442

His	Thr	Ile	Ile	Thr	Asp	Thr	Glu	Leu	Pro	Pro	Leu	Lys	Leu	Met	His		
10						15					20						
tca	ttt	tgt	gca	ttc	aag	tcg	gat	gat	ggc	cca	tgt	aaa	gca	atc	atg	490	
Ser	Phe	Cys	Ala	Phe	Lys	Ser	Asp	Asp	Gly	Pro	Cys	Lys	Ala	Ile	Met		
25					30				35						40		
aaa	aga	ttt	ttc	ttc	aat	att	ttc	act	cga	cag	tgc	gaa	gaa	ttt	ata	538	
Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu	Glu	Phe	Ile		
				45				50						55			
tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag	586	
Tyr	Gly	Gly		Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu		
				60				65					70				
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa	634	
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu		
		75					80					85					
gaa	gat	cct	gga	ata	tgt	cga	ggt	tat	att	acc	agg	tat	ttt	tat	aac	682	
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn		
	90					95					100						
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggt	gga	tgc	ctg	ggc	730	
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly		
105				110					115					120			
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa	778	
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu		
				125				130						135			
gat	ggt	ccg	aat	ggt	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat	826	
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn		
			140					145					150				
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	ggt	ccc	agc	ctt	874	
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu		
		155					160					165					
ttt	gaa	ttt	cac	ggt	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga	922	
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly		
	170				175					180							
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg	970	
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly		
	185				190					195					200		
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat	1018	
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn		
				205				210						215			
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggt	ttc	atc	1066	
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile		
			220					225					230				
caa	aga	ata	tca	aaa	gga	ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag	1114	
Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys		
		235				240						245					
aag	cag	aga	gtg	aaa	ata	gca	tat	gaa	gaa	att	ttt	ggt	aaa	aat	atg	1162	
Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met		
	250					255					260						
tgaatttggt	atagcaatgt	aacattaatt	ctactaaata	ttttatatga	aatgtttcac	1222											
tatgattttc	tattttttctt	ctaaaatgct	tttaattaat	atgttcatta	aatttttctat	1282											
gcttattgta	cttggttatca	aaaaaaaaaaaa	aaaaa			1317											

<210> 52

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..28

<400> 52

Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys

-25

-20

-15

Leu	Leu	Leu	Asn	Leu	Ala	Pro	Ala	Pro	Leu	Asn	Ala	Asp	Ser	Glu	Glu
	-10						-5					1			
Asp	Glu	Glu	His	Thr	Ile	Ile	Thr	Asp	Thr	Glu	Leu	Pro	Pro	Leu	Lys
5					10					15					20
Leu	Met	His	Ser	Phe	Cys	Ala	Phe	Lys	Ser	Asp	Asp	Gly	Pro	Cys	Lys
				25					30					35	
Ala	Ile	Met	Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu
			40					45					50		
Glu	Phe	Ile	Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser
		55					60					65			
Leu	Glu	Glu	Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys
	70					75					80				
Phe	Leu	Glu	Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr
85					90					95					100
Phe	Tyr	Asn	Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly
				105					110					115	
Cys	Leu	Gly	Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn
			120					125					130		
Ile	Cys	Glu	Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr
		135					140					145			
Gln	Leu	Asn	Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val
	150					155					160				
Pro	Ser	Leu	Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala
165					170					175					180
Asp	Arg	Gly	Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser
				185					190					195	
Val	Ile	Gly	Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn
			200					205					210		
Glu	Asn	Asn	Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys
		215					220					225			
Gly	Phe	Ile	Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg
	230					235					240				
Lys	Arg	Lys	Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val
245					250					255					260
Lys	Asn	Met													

<210> 53
 <211> 1907
 <212> DNA
 <213> Homo sapiens

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 <221> 5'UTR
 <222> 1..1043

<220>
 <221> CDS
 <222> 1044..1664

<220>
 <221> 3'UTR
 <222> 1665..1907

<220>
 <221> polyA_signal
 <222> 1869..1874

<220>
 <221> polyA_site
 <222> 1892..1907

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cctggacatt ttgggtattg tttcagtgga acatgccttt cataagttcc attttcttgg 120
gtatctctta ggaagcaagc ataggaaaca ggcccatccg tctgcctgtt ttgcttccctc 180
atctcacttc tacacgaggg tgccctgtgt caattgctgt tttcccctaa agagactctt 240
ttccataagt ttgtgaaatg ccatcgacaa acctgatcgc attgcatttc actctgtgtg 300
tgagtcgatt tttctttatt ttatcattta gtaactcctt gctctacaga gctttcacct 360
tccacatatt tcagattcat tctttcctaa actatgtggg ggtctacgtc ctactgact 420
tatcaacatg ctaccatcat gcacttctta tctctattcc tcttctttaa atttggttcc 480
aaatggctca caccattatt ctgagctatt acctgcctac gcagtcctag aaagtaagtg 540
attcaggaaa cattcccca aagtaaagt tctcaggtaa gatcagaaga ctcccatgag 600
tactgtctgc tcaggatcac atctggctcc ttgaagagt attcatcaga ccttacatag 660
atcttgtcat aaaaatgaaa gaggcctcgg gggaaggtct tgggctgggtg gcttctgttg 720
gagtcctggg ctgtgggggtg aaagccgtgg ctgtagagct tcatgcggag ttacttagct 780
ttgctctcct gtggacaggc catgcctgtg cctccccc aa gcatcggaaa aattggcata 840
gatggggcct tctcaaaaat cccactcctg gagcactggc caaaattact accatcctga 900
tgctgggctt gcagtccttt cctttgggaa tatgaacatg gtcaaaatta agtgaacgtg 960
tctttctggc tttctgtaca atggagcaga acaaagtatc aatttaacta aaatttgaac 1020
taaatcctct ttccagggtt gga atg cac ttc tgt gga ggc acc ttg ata tcc 1073
Met His Phe Cys Gly Gly Thr Leu Ile Ser
1 5 10
cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg 1121
Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg
15 20 25
cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc 1169
Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu
30 35 40
gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc 1217
Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro
45 50 55
aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc 1265
Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile
60 65 70
act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat gtg gtc 1313
Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val
75 80 85 90
gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc caa ggt 1361
Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly
95 100 105
act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag 1409
Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu
110 115 120
aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc 1457
Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser
125 130 135
acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag 1505
Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln
140 145 150
ggg gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att 1553
Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile
155 160 165 170
tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag 1601
Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys
175 180 185
cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga 1649
Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly
190 195 200
gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag 1704
Val Met Arg Asn Asn
205
aggctggaac gtgggtaggg atttagcatg ctggaaataa ctggcagtaa tcaaacgaag 1764
acactgtccc cagctaccag ctatgcaaaa cctcggcatt tttgtgtta ttttctgact 1824
gctggattct gtagtaaggg gacatagcta tgacatttgt taaaaataaa ctctgtactt 1884
aactttgaaa aaaaaaaaaa aaa 1907

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<210> 54
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 54
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 20 25 30
 Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
 35 40 45
 Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
 50 55 60
 Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
 65 70 75 80
 Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
 85 90 95
 Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
 100 105 110
 Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
 115 120 125
 Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
 130 135 140
 His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 145 150 155 160
 Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
 165 170 175
 Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
 180 185 190
 Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 195 200 205

<210> 55
 <211> 809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..25

<220>
 <221> CDS
 <222> 26..628

<220>
 <221> 3'UTR
 <222> 629..809

<220>
 <221> polyA_signal
 <222> 766..771

<220>
 <221> polyA_site
 <222> 795..809

<400> 55
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 Met Leu Glu Val Ser Asp Ala Leu Gly
 1 5
 gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac 100

Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp
 10 15 20 25
 acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148
 Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg
 30 35 40
 aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196
 Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro
 45 50 55
 ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc 244
 Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser
 60 65 70
 ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg 292
 Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val
 75 80 85
 ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca 340
 Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala
 90 95 100 105
 tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc 388
 Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala
 110 115 120
 ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat 436
 Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Glu Asp
 125 130 135
 ctg cag agg atc atc ctg cga ctg ctg aac agt gat gac atg tct gag 484
 Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu
 140 145 150
 gac ctc ctg atg gac ctc acg aac cac gtc ctg agt gag tgc gat ctg 532
 Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu
 155 160 165
 gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc 580
 Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala
 170 175 180 185
 aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc 628
 Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys
 190 195 200
 tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaacccc 688
 ctccagcact ggagggagct ggtttgaagt atgactttgt actggggcca cactcacctc 748
 tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaaaa aaaaaaaaaa 808
 t 809

<210> 56
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Leu Glu Val Ser Asp Ala Leu Gly Gly Pro Gly Arg Val Pro Gly
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 Ala Thr Ala Gly Met Asn Gly Val Asp Thr Ser Leu Leu Cys Asp Leu
 20 25 30
 Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His
 35 40 45
 Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Lys Glu Ala
 50 55 60
 Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn
 65 70 75 80
 Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe
 85 90 95
 Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala
 100 105 110
 Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn
 115 120 125
 Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg

130 135 140
 Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr
 145 150 155 160
 Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser
 165 170 175
 Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn
 180 185 190
 Ser Phe Arg Ile His Phe Trp Gly Cys
 195 200

<210> 57
 <211> 1133
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..475

<220>
 <221> CDS
 <222> 476..964

<220>
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 <222> 965..1133

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 <222> 1101..1106

<220>
 <221> polyA_site
 <222> 1118..1133

<400> 57
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 gagccaggag gtggcaggac gagttaggag gctgggttcag tagctcgggc aagagcaggg 120
 ccccccagga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg 180
 aggaccccaa ggtaactccg gtgagaaggg cgaccaggga tttcaaggcc agccaggctt 240
 tccgggcccc ccgggtcccc ctggattccc aggcaaagtt ggatcacctg gcccacctgg 300
 ccctcaagca gagaagggca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360
 tgggccaccg ggacctcctg ggattcaggg ccccgccggg ctggatggtt tggatgggaa 420
 ggatggcaag cctggcttga ggggggaccc tggtcctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
 50 55 60 65
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
 70 75 80
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly

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      85              90              95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg      814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
      100              105              110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc      862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
      115              120              125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc      910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
      130              135              140              145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct      958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
      150              155              160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg      1014
Phe Gly
ccaaagctta taggactctg tgacagggttg tgaatgtttt ttttgtgtgt gttgtgtgtt 1074
ttaattgctg ttaatatattt ttaaataata aagaacacaaa actaaaaaaaa aaaaaaaaaa 1133

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<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

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<400> 58
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Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
      20      25      30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
      35      40      45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
      50      55      60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
      65      70      75      80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
      85      90      95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
      100      105      110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
      115      120      125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
      130      135      140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
      145      150      155      160
Pro Phe Gly

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<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..78

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<220>
<221> CDS
<222> 79..642

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<220>
<221> 3'UTR
<222> 643..838

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<220>
 <221> polyA_signal
 <222> 799..804

<220>
 <221> polyA_site
 <222> 823..838

<400> 59
 aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggtc 60
 cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
 Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
 1 5 10
 aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
 Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
 15 20 25
 aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
 Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
 30 35 40
 gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
 Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
 45 50 55
 gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
 Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
 60 65 70 75
 gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
 Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
 80 85 90
 gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
 Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
 95 100 105
 gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
 Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
 110 115 120
 cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
 His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
 125 130 135
 gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
 Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
 140 145 150 155
 tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
 Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
 160 165 170
 gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
 Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
 175 180 185
 aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccaccct 692
 Lys
 gacccctccc tcagctgtcc tgtgccccgc cctctccgc acactcagtc cccctgctg 752
 gcgttcctgc cgcagctctg acctggtgct gtcgccctgg catcttaata aamcctgctt 812
 atacttcctt aaaaaaaaaa aaaaaa 838

<210> 60
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
 1 5 10 15
 Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
 20 25 30
 Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp

35 40 45
 Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
 50 55 60
 Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
 65 70 75 80
 Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
 85 90 95
 Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
 100 105 110
 Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
 115 120 125
 Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
 130 135 140
 Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
 145 150 155 160
 Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
 165 170 175
 Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
 180 185

<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..158

<220>
 <221> CDS
 <222> 159..764

<220>
 <221> 3'UTR
 <222> 765..862

<400> 61
 attttttttt ttggcacgcc tgcagccaag ttggggaggg tttcctggac agaggtcctt 60
 tggtgtctgc cttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggacccagac 120
 ccgctgcagg cagcagcagc ccccgcccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr

85	90	95	
gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc			560
Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly			
100	105	110	
ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc			608
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala			
115	120	125	130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat			656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp			
135	140	145	
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc			704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly			
150	155	160	
aag tgg ttc gac aag cgc tgc gcg gat cag ctg ccc tac atc tgc cag			752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln			
165	170	175	
ttc ggg atc gtg tagccggcgg ggcggggggcc gtggggggggc tggaggaggg			804
Phe Gly Ile Val			
180			
caggagccgc gggaggccgg gaggagggtg gggaccttgc agcccccac ctcctcgt			862

<210> 62
 <211> 202
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

<400> 62	
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu	
-20	-15
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val	
-5	5
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys	
15	20
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln	
30	35
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys	
45	50
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu	
60	65
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser	
80	85
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu	
95	100
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp	
110	115
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu	
125	130
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu	
140	145
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln	
160	165
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val	
175	180

<210> 63
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..194

<220>
 <221> CDS
 <222> 195..587

<220>
 <221> 3'UTR
 <222> 588..618

<220>
 <221> polyA_signal
 <222> 578..583

<220>
 <221> polyA_site
 <222> 604..618

<400> 63
 atttgcttag gtctgatcaa tctgctccac acaattttctc agtgatcctc tgcattctctg 60
 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
 ttcgttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
 -20 -15 -10
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
 -5 1 5
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
 10 15 20
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
 25 30 35
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
 40 45 50 55
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
 60 65 70
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
 75 80 85
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
 90 95 100
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
 Cys Phe Ala Leu Leu Asn Cys
 105 110

<210> 64
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

<400> 64
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly

	-20					-15						-10							
Leu	Ala	Ile	Leu	Ala	Ile	Leu	Leu	Thr	Arg	Trp	Ala	Arg	Arg	Lys	Gln				
	-5					1				5				10					
Ser	Glu	Met	His	Ile	Ser	Arg	Tyr	Ser	Ser	Glu	Gln	Ser	Ala	Arg	Leu				
			15						20					25					
Leu	Asp	Tyr	Glu	Asp	Gly	Arg	Gly	Ser	Arg	His	Ala	Tyr	Ser	Thr	Gln				
			30					35					40						
Ser	Glu	Arg	Ser	Lys	Arg	Asp	Tyr	Thr	Pro	Ser	Thr	Asn	Ser	Leu	Ala				
	45					50						55							
Leu	Ser	Arg	Ser	Ser	Ile	Ala	Leu	Pro	Gln	Gly	Ser	Met	Ser	Ser	Ile				
	60					65					70								
Lys	Cys	Leu	Gln	Thr	Thr	Glu	Glu	Leu	Pro	Ser	Arg	Thr	Ala	Gly	Ala				
	75				80						85				90				
Met	Ser	Lys	Phe	Phe	Phe	Cys	Pro	Leu	Ile	Leu	Met	Cys	Phe	Ala	Leu				
				95					100						105				

Leu Asn Cys

<210> 65
 <211> 836
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..176

<220>
 <221> CDS
 <222> 177..767

<220>
 <221> 3'UTR
 <222> 768..836

<220>
 <221> polyA_signal
 <222> 814..819

<220>
 <221> polyA_site
 <222> 822..836

<400> 65
 aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgcctacaag ggccctccctg 60
 acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
 ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg 179
 Met
 aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
 -20 -15 -10 -5
 gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
 Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
 1 5 10
 gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
 Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
 15 20 25
 gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
 Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
 30 35 40
 gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
 Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
 45 50 55 60
 tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467

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Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
      65      70      75
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
      80      85      90
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
      95      100      105
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
      110      115      120
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
      125      130      135      140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
      145      150      155
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
      160      165      170
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg 807
Phe Ser Pro Ala
      175
atagtgtata aatgaaaaaa aaaaaaaaaa 836

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<210> 66
<211> 197
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..22

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<400> 66
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
      -20      -15      -10
Leu Ala Ile Leu Ala Ile Leu Thr Arg Trp Ala Arg Arg Lys Gln
      -5      1      5      10
Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
      15      20      25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
      30      35      40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
      45      50      55
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
      60      65      70
Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
      75      80      85      90
Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
      95      100      105
Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
      110      115      120
Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
      125      130      135
Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
      140      145      150
Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
      155      160      165      170
Leu Phe Ser Pro Ala
      175

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<210> 67

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<211> 789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..789

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 774..789

<400> 67
 atatgtcatc aggccccccg cctgggaggt gtgctgccag agattttgcc ttttcaaggt 60
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
 caccccaatg ggaccacct cctgggtccc ctgggtgccgt ttttccttag aaatcagaga 712
 aatgggaaag ggggggaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
 gaaaaaaaa aaaaaaa 789

<210> 68
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
 1 5 10 15
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 69
 <211> 2556
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..66

<220>
 <221> CDS
 <222> 67..2427

<220>
 <221> 3'UTR
 <222> 2428..2556

<220>
 <221> polyA_signal
 <222> 2522..2527

<220>
 <221> polyA_site
 <222> 2541..2556

<400> 69
 gtccccgcgt ccctggcaat tcccgaattc ccaacggctt cctgctggca gccccgaagc 60
 cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
 Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu
 -15 -10 -5
 ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
 Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
 1 5 10 15

cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat	204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr	
20 25 30	
gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg	252
Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val	
35 40 45	
cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg	300
His Leu Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu	
50 55 60	
tac aat caa gga tct atg aat act tat tct tca gat att cag act caa	348
Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln	
65 70 75	
tgc tac tat caa gga aat att gaa gaa tat cca gat tcc atg gtc aca	396
Cys Tyr Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr	
80 85 90 95	
ctc agc acg tgc tct gga cta aga gga ata ctg caa ttt gaa aat gtt	444
Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val	
100 105 110	
tct tat gga att gag cct ctg gaa tct gca gtt gaa ttt cag cat gtt	492
Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val	
115 120 125	
ctt cac aaa tta aag aat gaa gac aat gat att gca att ttt att gac	540
Leu His Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp	
130 135 140	
aga agc ctg aaa gaa caa cca atg gat gac aac att ttt ata agt gaa	588
Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu	
145 150 155	
aaa tca gaa cca gct gtt cca gat tta ttt cct ctt tat cta gaa atg	636
Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met	
160 165 170 175	
cat att gtg gtg gac aaa act ttg tat gat tac tgg ggc tct gat agc	684
His Ile Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser	
180 185 190	
atg ata gta aca aat aaa gtc atc gaa att gtt ggc ctt gca aat tca	732
Met Ile Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser	
195 200 205	
atg ttc acc caa ttt aaa gtt act att gtg ctg tca tca ttg gag tta	780
Met Phe Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu	
210 215 220	
tgg tca gat gaa aat aag att tct aca gtt ggt gag gca gat gaa tta	828
Trp Ser Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu	
225 230 235	
ttg caa aaa ttt tta gaa tgg aaa caa tct tat ctt aac cta agg cct	876
Leu Gln Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro	
240 245 250 255	
cat gat att gca tat cta cta att tat atg gat tat cct cgt tat ttg	924
His Asp Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu	
260 265 270	
gga gca gtg ttt cct gga aca atg tgt att act cgt tat tct gca gga	972
Gly Ala Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly	
275 280 285	
gtc gca ttg tac ccc aag gag ata act ctg gag gca ttt gca gtt att	1020
Val Ala Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile	
290 295 300	
gtc acc cag atg ctg gca ctc agt ctg gga ata tca tat gac gac cca	1068
Val Thr Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro	
305 310 315	
aag aaa tgt caa tgt tca gaa tcc acc tgt ata atg aat cca gaa gtt	1116
Lys Lys Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val	
320 325 330 335	
gtg caa tcc aat ggt gtg aag act ttt agc agt tgc agt ttg agg agc	1164
Val Gln Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser	
340 345 350	

ttt	caa	aat	ttc	att	tca	aat	gtg	ggt	gtc	aaa	tgt	ctt	cag	aat	aag	1212
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
			355					360					365			
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
		370					375					380				
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggt	act	gag	gct	caa	tgt	gga	1308
Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	
	385					390					395					
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	
400					405					410					415	
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	
			420					425						430		
ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	
			435					440					445			
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggt	cct	gac	ata	act	tta	atc	1500
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	
		450					455						460			
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	
	465					470					475					
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggt	tca	1596
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	
480					485					490					495	
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	
			500					505						510		
aga	ttt	ggg	aac	tgt	ggt	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys	
			515					520						525		
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	
	530						535						540			
cga	aag	cct	ttc	cat	caa	gaa	aat	ggt	gat	gtg	att	tat	gct	ttc	gta	1788
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	
	545					550							555			
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	
560					565					570					575	
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884
Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg	
			580					585						590		
gtt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser	
			595					600						605		
gca	cat	gtt	tgt	tca	caa	cag	tgt	tct	gga	cat	gga	gtg	tgt	gat	tcc	1980
Ala	His	Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser	
		610					615							620		
aga	aac	aag	tgc	cat	tgt	tgc	cca	ggc	tat	aag	cct	cca	aac	tgc	caa	2028
Arg	Asn	Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Asn	Cys	Gln	
	625					630					635					
ata	cgt	tcc	aaa	gga	ttt	tcc	ata	ttt	cct	gag	gaa	gat	atg	ggt	tca	2076
Ile	Arg	Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser	
640					645					650					655	
atc	atg	gaa	aga	gca	tct	ggg	aag	act	gaa	aac	acc	tgg	ctt	cta	ggg	2124
Ile	Met	Glu	Arg	Ala	Ser	Gly	Lys	Thr	Glu	Asn	Thr	Trp	Leu	Leu	Gly	
			660					665						670		
ttc	ctc	att	gct	ctt	cct	att	ctc	att	gta	aca	acc	gca	ata	gtt	ttg	2172
Phe	Leu	Ile	Ala	Leu	Pro	Ile	Leu	Ile	Val	Thr	Thr	Ala	Ile	Val	Leu	
			675					680						685		

gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca 2220
Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro
690 695 700
agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa 2268
Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln
705 710 715
tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
720 725 730 735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
740 745 750
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
755 760 765
caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
Gln Ser Ser Ser Asn
770
tcgctaagaa atgaaaattc tgtctttcct tccgtggtca cagctgaaag aaacaataaa 2527
ttgagtggtg accaaaaaaa aaaaaaaat 2556

<210> 70
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<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..16

<400> 70
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-15 -10 -5
Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
1 5 10 15
Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
20 25 30
Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
35 40 45
Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
50 55 60
Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
65 70 75 80
Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
85 90 95
Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
100 105 110
Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
115 120 125
Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
130 135 140
Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
145 150 155 160
Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
165 170 175
Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
180 185 190
Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
195 200 205
Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
210 215 220
Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
225 230 235 240

Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
 245 250 255
 Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
 260 265 270
 Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
 275 280 285
 Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr
 290 295 300
 Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys
 305 310 315 320
 Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln
 325 330 335
 Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln
 340 345 350
 Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln
 355 360 365
 Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu
 370 375 380
 Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala
 385 390 395 400
 Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys
 405 410 415
 Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val
 420 425 430
 Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys
 435 440 445
 Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly
 450 455 460
 Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His
 465 470 475 480
 Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn
 485 490 495
 Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe
 500 505 510
 Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp
 515 520 525
 Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys
 530 535 540
 Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp
 545 550 555 560
 Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp
 565 570 575
 Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys
 580 585 590
 Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His
 595 600 605
 Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn
 610 615 620
 Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg
 625 630 635 640
 Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met
 645 650 655
 Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu
 660 665 670
 Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg
 675 680 685
 Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser
 690 695 700
 Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
 705 710 715 720
 Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser
 725 730 735
 Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu

740 745 750
 Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser
 755 760 765
 Ser Ser Asn
 770

<210> 71
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..7

<220>
 <221> CDS
 <222> 8..763

<220>
 <221> 3'UTR
 <222> 764..1603

<220>
 <221> polyA_signal
 <222> 1562..1567

<220>
 <221> polyA_site
 <222> 1588..1603

<400> 71
 gagaagg atg ggg ccg cat cta cac ctg tgc ctg tgt gtg cct gac ctg 49
 Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu
 -15 -10 -5
 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
 1 5 10
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
 15 20 25 30
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
 35 40 45
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
 50 55 60
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
 65 70 75
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
 80 85 90
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His
 95 100 105 110
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
 115 120 125
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
 130 135 140
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529

Leu	Val	Ala	Leu	Gly	Pro	Gly	His	Gly	Leu	Gln	Gly	Pro	His	Xaa	Ala	
	145						150					155				
ctc	ctg	gct	gca	atg	ctt	cgg	ggg	ctg	gca	ggg	ggc	cga	gtc	ctg	gcc	577
Leu	Leu	Ala	Ala	Met	Leu	Arg	Gly	Leu	Ala	Gly	Gly	Arg	Val	Leu	Ala	
	160					165					170					
ctc	ctg	gag	gag	aac	tcc	aca	ccc	cag	cta	gca	ggg	atc	ctg	gcc	cgg	625
Leu	Leu	Glu	Glu	Asn	Ser	Thr	Pro	Gln	Leu	Ala	Gly	Ile	Leu	Ala	Arg	
	175				180					185				190		
gtg	ctg	aat	gga	gag	gca	cct	cct	agc	cta	ggc	cct	tcc	tct	gtg	gcc	673
Val	Leu	Asn	Gly	Glu	Ala	Pro	Pro	Ser	Leu	Gly	Pro	Ser	Ser	Val	Ala	
			195					200						205		
tcc	cca	gag	gac	gtc	cag	gcc	ctg	atg	tac	ctg	aga	ggg	cag	ctg	gag	721
Ser	Pro	Glu	Asp	Val	Gln	Ala	Leu	Met	Tyr	Leu	Arg	Gly	Gln	Leu	Glu	
		210						215					220			
cct	cag	tgg	aag	atg	ttg	cag	tgc	cat	cct	cac	ctg	gtg	gct			763
Pro	Gln	Trp	Lys	Met	Leu	Gln	Cys	His	Pro	His	Leu	Val	Ala			
	225					230					235					
tgaaatcggc	caaggtggga	gcatttacac	cgcagaaatg	acaccgcacg	ccagcgcgcc											823
gcggccgcga	tccggacccc	aagcccacgg	ctccctcgac	tctggggcac	ggaaccccgc											883
ccactcccaa	tccccgcgcc	cgccctctc	ccaccctgc	ttcccccgct	ccacccctca											943
cctcacctcg	ccccgcgcgc	acccatcgcg	ccccggcgcg	tggtattgtt	cggtctgggt											1003
cggctcggcg	ctgtctccct	cggctctgcg	gggtgtcagtt	cgtccggctt	cctcacagcc											1063
cctcactccc	ggcggctgac	agcagcagcg	gcggcgcgcg	gcggcgcgctg	gcgtttcgag											1123
gctgagcggc	accgggggtt	gggcgcggag	gaggagcagc	agcgggagga	ggagccgtgt											1183
gccctggcac	tgagcggccg	cggccatggc	gtacgcctat	ctcttcaagt	acatcataat											1243
cggcgacaca	ggtgttggt	aatcatgctt	attgtctacag	tttacagaca	agaggttcag											1303
ccagtgcatt	accttactat	tggtgtagag	ttcggtgctc	gaatgataac	tattgatggg											1363
aaacagataa	aacttcagat	atgggatacg	gcagggcaag	aatcctttcg	ttccatcaca											1423
aggctgtatt	acagaggtgc	agcaggagct	ttactagtgt	acgatattac	acggagagat											1483
acattcaacc	acttgacaac	ctgggttagaa	gatgcccgcc	agcattccaa	ttccaacatg											1543
gtcattatgc	ttattggaaa	taaaagtgat	ttagaatcta	gaagaaaaaa	aaaaagaaaa											1603

<210> 72
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<220>
 <221> UNSURE
 <222> 173
 <223> Xaa = Ala,Gly

<400> 72
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 -15 -10 -5
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 1 5 10 15
 Ser Leu Ala Arg Glu Ala Leu Thr Ala Leu Gly Lys Leu Leu Tyr
 20 25 30
 Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile Ala Ala
 35 40 45
 Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val Arg Arg
 50 55 60
 Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu Gly Gln
 65 70 75
 Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu Trp Leu
 80 85 90 95
 Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His Val Ser
 100 105 110


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ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac 435
Ile Phe Ile
rtttctgttt wccttttagc aaggtgaaac cagtctggam aatggggaga tggggccgggt 495
gcagtggctc acattttaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtgggtggc 615
tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcaccctggc 675
caacatgggtg aaaccccgtc ttactaaaa atagaaaatt agccgggcgt gatggcacac 735
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795
gaggttgctg tgagtggaga tcatgccatt gcactccage ctgagcaaca agagcaaac 855
tccatcccaa aaaaaaaaaa aaaa 879

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<210> 74
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..16

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<400> 74
Met Ala Val Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly Pro Gly
  -15          -10          -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
  1           5           10          15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
  20          25          30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
  35          40          45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
  50          55          60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
  65          70          75          80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
  85          90          95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
  100         105         110
Ile

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<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..87

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<220>
<221> CDS
<222> 88..1269

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<220>
<221> 3'UTR
<222> 1270..1634

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<220>
<221> polyA_signal
<222> 1594..1599

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<220>
<221> polyA_site
<222> 1619..1634

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<400> 75

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aaagttcttc agcccttggc tcctgcccag tgtttagggg gttggcggag acaaagggga 60
agagtcacgc cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
Met Met Gly Val Phe Val Val Ala Ala
1 5
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162
Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
10 15 20 25
gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
30 35 40
aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258
Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
45 50 55
cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306
Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg
60 65 70
gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354
Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys
75 80 85
ggg tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402
Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val
90 95 100 105
aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450
Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln
110 115 120
gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498
Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser
125 130 135
gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat 546
Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His
140 145 150
gtc cag ctc ccc atg gca atg act gca gag aat ctt gct gta aaa cac 594
Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His
155 160 165
aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag 642
Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln
170 175 180 185
aga tgg aaa gct gct aat gat gct ggc tac ttt aat gat gaa atg gca 690
Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala
190 195 200
cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac 738
Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp
205 210 215
gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct 786
Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro
220 225 230
cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tcg ggt 834
Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly
235 240 245
gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt 882
Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val
250 255 260 265
aag aaa cat aac ttc aca cca ctg gca aga att gtg ggc tac ttt gta 930
Lys Lys His Asn Phe Thr Pro Leu Ala Arg Ile Val Gly Tyr Phe Val
270 275 280
tct gga tgt gat ccc tct atc atg ggt att ggt cct gtc cct gct atc 978
Ser Gly Cys Asp Pro Ser Ile Met Gly Ile Gly Pro Val Pro Ala Ile
285 290 295
agt ggg gca ctg aag aaa gca gga ctg agt ctt aag gac atg gat ttg 1026
Ser Gly Ala Leu Lys Lys Ala Gly Leu Ser Leu Lys Asp Met Asp Leu
300 305 310
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gta gag gtg aat gaa gct ttt gct ccc cag tac ttg gct gtt gag agg 1074
 Val Glu Val Asn Glu Ala Phe Ala Pro Gln Tyr Leu Ala Val Glu Arg
 315 320 325
 agt ttg gat ctt gac ata agt aaa acc aat gtg aat gga gga gcc att 1122
 Ser Leu Asp Leu Asp Ile Ser Lys Thr Asn Val Asn Gly Gly Ala Ile
 330 335 340 345
 gct ttg ggt cac cca ctg gga gga tct gga tca aga att act gca cac 1170
 Ala Leu Gly His Pro Leu Gly Gly Ser Gly Ser Arg Ile Thr Ala His
 350 355 360
 ctg gtt cac gaa tta agg cgt cga ggt gga aaa tat gcc gtt gga tca 1218
 Leu Val His Glu Leu Arg Arg Arg Gly Gly Lys Tyr Ala Val Gly Ser
 365 370 375
 gct tgc att gga ggt ggc caa ggt att gct gtc atc att cag agc aca 1266
 Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr
 380 385 390
 gcc tgaagagacc agtgagctca ctgtgaccca tccttactct acttggccag 1319
 Ala
 gccacagtaa aacaagtgac cttcagagca gctgccacaa ctggccatgc cctgccattg 1379
 aaacagtgat taagtttgat caagccatgg tgacacaaaa atgcattgat catgaatagg 1439
 agcccatgct agaagtacat tctctcagat ttgaaccagt gaaatatgat gtatttctga 1499
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 aaaaaaaaaa aaaaa 1634

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 <211> 394
 <212> PRT
 <213> Homo sapiens

<400> 76
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 Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro Glu Thr Val
 35 40 45
 Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile
 50 55 60
 Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr
 65 70 75 80
 Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile
 85 90 95
 Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu
 100 105 110
 Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn
 115 120 125
 Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser
 130 135 140
 Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met
 145 150 155 160
 Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys
 165 170 175
 Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp
 180 185 190
 Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys
 195 200 205
 Lys Gly Lys Gln Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr
 210 215 220
 Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly
 225 230 235 240
 Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala
 245 250 255
 Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro

	260		265		270										
Leu	Ala	Arg	Ile	Val	Gly	Tyr	Phe	Val	Ser	Gly	Cys	Asp	Pro	Ser	Ile
	275		280		285										
Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Ile	Ser	Gly	Ala	Leu	Lys	Lys	Ala
	290		295		300										
Gly	Leu	Ser	Leu	Lys	Asp	Met	Asp	Leu	Val	Glu	Val	Asn	Glu	Ala	Phe
305				310						315					320
Ala	Pro	Gln	Tyr	Leu	Ala	Val	Glu	Arg	Ser	Leu	Asp	Leu	Asp	Ile	Ser
			325						330					335	
Lys	Thr	Asn	Val	Asn	Gly	Gly	Ala	Ile	Ala	Leu	Gly	His	Pro	Leu	Gly
		340						345					350		
Gly	Ser	Gly	Ser	Arg	Ile	Thr	Ala	His	Leu	Val	His	Glu	Leu	Arg	Arg
		355					360					365			
Arg	Gly	Gly	Lys	Tyr	Ala	Val	Gly	Ser	Ala	Cys	Ile	Gly	Gly	Gly	Gln
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Gly	Ile	Ala	Val	Ile	Ile	Gln	Ser	Thr	Ala						
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 <213> Homo sapiens

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 <222> 1599..1604

<220>
 <221> polyA_site
 <222> 1627..1642

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 Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
 -20 -15 -10
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 Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
 -5 1 5 10
 gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc 206
 Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
 15 20 25
 gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg 254
 Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu
 30 35 40
 aag gag gac gcg ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc 302
 Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
 45 50 55
 gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg 350
 Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
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ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
75 80 85 90
aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446
Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
95 100 105
aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc 494
Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile
110 115 120
act gac tct gag gac aag gcc ctc atg aac ggc tcc gag agc agg ttc 542
Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe
125 130 135
ttc gtg agt tcc tcg cag ggc ctg tca gag cta cac att gag aac ctg 590
Phe Val Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu
140 145 150
aac atg gag gcc gac ccc ggc cag tac cgg tgc aac ggc acc agc tcc 638
Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser
155 160 165 170
aag ggc tcc gac cag gcc atc atc acg ctc cgc gtg cgc agc cac ctg 686
Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu
175 180 185
gcc gcc ctc tgg ccc ttc ctg ggc atc gtg gct gag gtg ctg gtg ctg 734
Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu
190 195 200
gtc acc atc atc ttc atc tac gag aag cgc cgg aag ccc gag gac gtc 782
Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val
205 210 215
ctg gat gat gac gac gcc ggc tct gca ccc ctg aag agc agc ggg cag 830
Leu Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln
220 225 230
cac cag aat gac aaa ggc aag aac gtc cgc cag agg aac tct tcc 875
His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
235 240 245
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cccagtgctt gcaagattcc aagttctcac ctcttaaaga aaaccacccc cgtagattcc 995
catcatacac ttccttcttt tttaaaaaag ttgggttttc tccattcagg attctgttcc 1055
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<210> 78
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

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 His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
 -5 1 5 10
 Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
 15 20 25

Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
 30 35 40
 Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
 45 50 55
 Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
 60 65 70 75
 Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
 80 85 90
 Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
 95 100 105
 Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
 110 115 120
 Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
 125 130 135
 Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met
 140 145 150 155
 Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
 160 165 170
 Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
 175 180 185
 Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
 190 195 200
 Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
 205 210 215
 Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
 220 225 230 235
 Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
 240 245

<210> 79
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 <212> DNA
 <213> Homo sapiens

<220>
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<220>
 <221> CDS
 <222> 344..1144

<220>
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 <222> 1145..1466

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 ggagcagagg tggccggcgg gcccggtga ctgcgcctyt gctttctttc cataaccttt 240
 tctttcggac tcgaatcacg gctgctgcga aggtctagt tccggacact agggtgcccg 300
 aacgcgctga tgccccgagt gctcgcaggg cttcccgtta acc atg ctg ccg ccg 355
 Met Leu Pro Pro
 ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403
 Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu
 -25 -20 -15 -10
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 Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro
 -5 1 5
 gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc 499
 Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly
 10 15 20

tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg 547
Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu
25 30 35
gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac 595
Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn
40 45 50 55
ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct cac ttc tac ggg 643
Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala His Phe Tyr Gly
60 65 70
cac tgc ggc gag cag ctt gag tgc cgg ctg gac aca ggc ggc gac ctg 691
His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr Gly Gly Asp Leu
75 80 85
agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgt cgt tcg cag agt 739
Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys Arg Ser Gln Ser
90 95 100
ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag atc tgc cgc ctg 787
Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln Ile Cys Arg Leu
105 110 115
cag gag gcg gcc cgc gct cgg ccc gat gcc aac ctc act gtg gca cac 835
Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu Thr Val Ala His
120 125 130 135
ccg ggg ccc tgc gaa tcg ggg ccc cag atc gtg tca cat cca tat gac 883
Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser His Pro Tyr Asp
140 145 150
act tgg aat gtg aca ggg cag gat gtg atc ttt ggc tgt gaa gtg ttt 931
Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly Cys Glu Val Phe
155 160 165
gcc tac ccc atg gcc tcc atc gag tgg agg aag gat ggc ttg gac atc 979
Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu Asp Ile
170 175 180
cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg ggt gga 1027
Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly
185 190 195
ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct gtg cgt 1075
Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg
200 205 210 215
ccc agt gat gag ggc act tac cgc tgc ctt ggc cca atg ccc tgg gtc 1123
Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro Met Pro Trp Val
220 225 230
aag tgg agg ccc ctg cta gct tgacagtgtcacacctgac cagctgaact 1174
Lys Trp Arg Pro Leu Leu Ala
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ctacaggcat cccccagctg cgatcactaa acctggttcc tgaggaggag gctgagagtg 1234
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tgctttcatg ctgtcagtag ggatgatcat gggaggccta tttgactcca aggtagcagt 1414
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<211> 267
<212> PRT
<213> Homo sapiens

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<222> 1..30

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-10 -5 1
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Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys
 -5 1 5 10
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 Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp
 15 20 25
 tgc aca aca aat ttc tcc tgt acc tat ggg aag cct gtc act ttt gac 245
 Cys Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp
 30 35 40
 tgt gca gtg aaa cca tct gtt acc tgt gtt gat caa gac ttc aaa tcc 293
 Cys Ala Val Lys Pro Ser Val Thr Cys Val Asp Gln Asp Phe Lys Ser
 45 50 55
 caa aag aac ttc atc att aac atg act tgc aga ttt tgc tgg cag ctt 341
 Gln Lys Asn Phe Ile Ile Asn Met Thr Cys Arg Phe Cys Trp Gln Leu
 60 65 70
 cct gaa aca gat tac gag tgt acc aac tcc acc agc tgc atg acg gtg 389
 Pro Glu Thr Asp Tyr Glu Cys Thr Asn Ser Thr Ser Cys Met Thr Val
 75 80 85 90
 tcc tgt cct cgg cag cgc tac cct gcc aac tgc acg gtg cgg gac cac 437
 Ser Cys Pro Arg Gln Arg Tyr Pro Ala Asn Cys Thr Val Arg Asp His
 95 100 105
 gtc cac tgc ttg ggt aac cgt act ttt ccc aaa atg cta tat tgc aat 485
 Val His Cys Leu Gly Asn Arg Thr Phe Pro Lys Met Leu Tyr Cys Asn
 110 115 120
 tgg act gga ggc tat aag tgg tct acg gct ctg gct cta agc atc acc 533
 Trp Thr Gly Gly Tyr Lys Trp Ser Thr Ala Leu Ala Leu Ser Ile Thr
 125 130 135
 ctc ggt ggg ttt gga gca gac cgt ttc tac ctg ggc cag tgg cgg gaa 581
 Leu Gly Gly Phe Gly Ala Asp Arg Phe Tyr Leu Gly Gln Trp Arg Glu
 140 145 150
 ggc ctc ggc aag ctc ttc agc ttc ggt ggc ctg gga ata tgg acg ctg 629
 Gly Leu Gly Lys Leu Phe Ser Phe Gly Gly Leu Gly Ile Trp Thr Leu
 155 160 165 170
 ata gac gtc ctg ctc att gga gtt ggc tat gtt gga cca gca gat ggc 677
 Ile Asp Val Leu Leu Ile Gly Val Gly Tyr Val Gly Pro Ala Asp Gly
 175 180 185
 tct ttg tac att tagctgtggt gtgtgcttca gaaaggagca gggcttagaa 729
 Ser Leu Tyr Ile
 190
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 gtacagcatc tgtactttgt ttgccttgat aaaggtaaga taaatgaaac gctgaactat 849
 gctaactctgg aatttgtttt tatttgctg aaatataatt ttttctgtga aaaaattaaa 909
 acgtacttaa gccaggagaa tgaattatac agtgattgaa aatccattta attcctatga 969
 cttttgtttt gtattgccca agtcaaacta catcacttgt atctccagcc caaatgtagt 1029
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..32

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 1 5 10 15
 Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys
 20 25 30
 Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
 35 40 45
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
 50 55 60
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
 65 70 75 80
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
 85 90 95
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
 100 105 110
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
 115 120 125
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
 130 135 140
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
 145 150 155 160
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
 165 170 175
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<210> 83
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 <212> DNA
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 <221> CDS
 <222> 118..510

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 <221> 3'UTR
 <222> 511..1754

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<220>
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 <222> 1739..1754

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 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
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 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
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 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala

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10          15          20          25
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Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          30          35          40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
          75          80          85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
          90          95          100          105
ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550
Gly Pro Ser
acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacgcc 610
gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
cgggcccctc cccggccctc cggcctgccc ggcaccccgc gacccctgg ccccgcgggc 730
tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
gacgagaagt cgaggctctt tatgsacgcg cggcacaagc ggggacgcgc agacatccgc 850
gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg cgtgcggag ccacacgcgc 910
accgagtgca aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
ctgcctccat ttcgcgaggt gggcgcgcgcg ctgctggagc gcttccacgg cgcctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgcgc tccgcacgct caagccgcgc 1090
ggccgagcgg acctcctcta cgccgccgat tcgcccgaact tctgcgcccc caaccgacgc 1150
accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgctgcgg ccgcgggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgctgtgcc gcttccactg gtgctgcgta gtacagtgc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgctgtg acccgccgcc cggccgctag actgacttcg cgcagcggtg 1390
gctcgcacct gtgggacctc agggcacccg caccgggcgc ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacaag gccagggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg aactgtaca ggccctccct ccccttgccc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatattt aaaccaccaa aaaaaaaaaa 1750
aaaaa 1754

```

```

<210> 84
<211> 131
<212> PRT
<213> Homo sapiens

```

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<220>
<221> SIGNAL
<222> 1..24

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<400> 84
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
          10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu

```

```

          75          80          85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
          90          95          100
Gly Pro Ser
105

```

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<210> 85
<211> 1754
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..117

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<220>
<221> CDS
<222> 118..510

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<220>
<221> 3'UTR
<222> 511..1754

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<220>
<221> polyA_signal
<222> 1718..1723

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<220>
<221> polyA_site
<222> 1739..1754

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<400> 85
tccccggccg ccgccgttgc gctcgccgcg ctgcactga agccccgggcc ctgcgcgcc 60
gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctg ggg ctg ctg ctg ctg ctg 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
          -20          -15          -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10          15          20          25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          30          35          40
ctg gct cgg ggc gcc cgg ctg ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60          65          70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
75          80          85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90          95          100          105
ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcatte 550
Gly Pro Ser
acagacattc gggagacggc cttcgtgttc gccatcactg cgcccgggcg cagccacgcc 610
gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
cgggccctc ccggccctc cggcctgccc ggcacccccg gacccctgg ccccgcgggc 730

```

```

tccccggaag gcagcgccgc ctgggagtg ggaggctgcg gcgacgacgt ggacttcggg 790
gacgagaagt cgaggtctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
accgagtgca aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
ctgcctccat ttcgcgaggt gggcgcgcg cgctgggagc gcttycacgg cgctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgcg tccgcacgct caagccgcgc 1090
ggccgagcgg acctcctcta cgccgccgat tcgcccgact tctgcgcccc caaccgacgc 1150
accggtcccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgctgcgg ccgcgggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgccgtgccc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgcctgtg acccgccgcc cggccgctag actgacttcg cgcagcgggtg 1390
gctgcacact gtgggacctc agggcaccgg caccggcgcg ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gcccaggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg aactgtaca ggcctccct ccccttgccc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatattt aaaccaccaa aaaaaaaaaa 1750
aaaa
1754

```

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<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
      -20                      -15                      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5                      1                      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10                      15                      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25                      30                      35                      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45                      50                      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60                      65                      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
      75                      80                      85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
      90                      95                      100
Gly Pro Ser
105

```

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<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..151

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<220>
<221> CDS
<222> 152..655

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<220>
<221> 3'UTR

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<222> 656..1431

<220>

<221> polyA_signal

<222> 1399..1404

<220>

<221> polyA_site

<222> 1416..1431

<400> 87

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gcccaaacca agggccccag agaggctccc caggcccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                               Met Leu Phe Arg Leu Ser Glu
                               1 5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
10 15 20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
25 30 35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
40 45 50 55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
60 65 70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
75 80 85
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
90 95 100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
105 110 115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
120 125 130 135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
140 145 150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
155 160 165
aca taggcaccca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr
tccccagaaa cccactctat cctcacccctg ttttgtgctc ttccccctgc ctgctagggc 765
tgcggctttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccacacctt 825
ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccacctctgc cagtcattcc 885
tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945
gggaacaggg atttgccctt cacaattcta ctccccagat cctctccccct ggacacagga 1005
gacccacagg gcaggacctt aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctaccca ctttctatg gaggattcca agtcaccact tctctcaccg 1125
gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tgttgcggtt tgtgctttga tgccaggaat gccgectagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccagggt ttccttgtcc cccagctgct ctgccccctt ccccttcttc 1365
cctgactcca ggcctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa 1431
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<210> 88

<211> 168
 <212> PRT
 <213> Homo sapiens

<400> 88

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Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1          5          10          15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
          20          25          30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
          35          40          45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
          50          55          60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65          70          75          80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
          85          90          95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
          100         105         110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
          115         120         125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
          130         135         140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145         150         155         160
Pro Ser Pro Ser Glu Pro Gly Thr
          165
  
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<210> 89
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

<400> 89

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aatttttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa   60
gcccaaacca aggcccccag agaggtcccc caggcccctt tgggtccctg agcctcagct   120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag   172
          Met Leu Phe Arg Leu Ser Glu
          1          5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga   220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
          10          15          20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca   268
  
```

Glu	Gly	His	His	Leu	Lys	Ser	Lys	Arg	Pro	Asn	Pro	Cys	Ala	Tyr	Thr		
25						30				35							
cca	cct	tcg	ctg	aaa	gct	gtg	cag	cgc	att	gct	gag	tct	cac	ctg	cag	316	
Pro	Pro	Ser	Leu	Lys	Ala	Val	Gln	Arg	Ile	Ala	Glu	Ser	His	Leu	Gln		
40				45						50					55		
tct	atc	agc	aat	ttg	aat	gag	aac	cag	gcc	tca	gag	gag	gag	gat	gag	364	
Ser	Ile	Ser	Asn	Leu	Asn	Glu	Asn	Gln	Ala	Ser	Glu	Glu	Glu	Asp	Glu		
			60						65					70			
ctg	ggg	gag	ctt	cgg	gag	ctg	ggt	tat	cca	aga	gag	gaa	gat	gag	gag	412	
Leu	Gly	Glu	Leu	Arg	Glu	Leu	Gly	Tyr	Pro	Arg	Glu	Glu	Asp	Glu	Glu		
			75					80					85				
gaa	gag	gag	gat	gat	gaa	gaa	gag	gaa	gaa	gaa	gag	gac	agc	cag	gct	460	
Glu	Glu	Glu	Asp	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Ser	Gln	Ala		
			90				95					100					
gaa	gtc	ctg	aag	gtc	atc	agg	cag	tct	gct	ggg	caa	aag	aca	acc	tgt	508	
Glu	Val	Leu	Lys	Val	Ile	Arg	Gln	Ser	Ala	Gly	Gln	Lys	Thr	Thr	Cys		
	105					110					115						
ggc	cag	ggt	ctg	gaa	ggg	ccc	tgg	gag	cgc	cca	ccc	cct	ctg	gat	gag	556	
Gly	Gln	Gly	Leu	Glu	Gly	Pro	Trp	Glu	Arg	Pro	Pro	Pro	Leu	Asp	Glu		
			120		125					130				135			
tcc	gag	aga	gat	gga	ggc	tct	gag	gac	caa	gtg	gaa	gac	cca	gca	cta	604	
Ser	Glu	Arg	Asp	Gly	Gly	Ser	Glu	Asp	Gln	Val	Glu	Asp	Pro	Ala	Leu		
			140						145					150			
agt	gag	cct	ggg	gag	gaa	cct	cag	cgc	cct	tcc	ccc	tct	gag	cct	ggc	652	
Ser	Glu	Pro	Gly	Glu	Glu	Pro	Gln	Arg	Pro	Ser	Pro	Ser	Glu	Pro	Gly		
			155					160					165				
aca	taggcaccca	gcctgcatct	cccaggagga	agtgaggagg	acatcgctgt											705	
Thr																	
tccccagaaa	cccactctat	cctcaccctg	ttttgtgctc	ttcccctcgc	ctgctagggc	765											
tgcggtcttct	gacttctaga	agactaaggc	tggtctgtgt	ttgcttggtt	gcccaccttt	825											
ggctgatacc	cagagaacct	gggcacttgc	tgctctgatgc	ccaccctcgc	cagtcattcc	885											
tccattcacc	cagcgggagg	tgggatgtga	gacagccac	attggaaaat	ccagaaaacc	945											
gggaacaggg	atttgccctt	cacaattcta	ctccccagat	cctctcccct	ggacacagga	1005											
gacccacagg	gcaggacct	aagatctggg	gaaaggagg	cctgagaacc	ttgaggtacc	1065											
cttagatcct	tttctaccca	ctttcctatg	gaggattcca	agtcaccact	tctctaccg	1125											
gcttctacca	gggtccagga	ctaaggcgtt	tttctccata	gcctcaacat	tttggaatc	1185											
ttccctaat	cacccttgct	cctcctgggt	gcctggaaga	tggaactggca	gagacctctt	1245											
tggtgcgttt	tgtgctttga	tgccaggaat	cccgcctagt	ttatgtcccc	ggtggggcac	1305											
acagcggggg	gcgccaggtt	ttccttgctc	cccagctgct	ctgccccttt	cccctcttc	1365											
cctgactcca	ggcctgaacc	cctcccgtgc	tgtaataaat	ctttgtaaag	aaaaaaaaa	1425											
aaaaaa						1431											

<210> 90

<211> 168

<212> PRT

<213> Homo sapiens

<400> 90

Met	Leu	Phe	Arg	Leu	Ser	Glu	His	Ser	Ser	Pro	Glu	Glu	Glu	Ala	Ser		
1				5					10					15			
Pro	His	Gln	Arg	Ala	Ser	Gly	Glu	Gly	His	His	Leu	Lys	Ser	Lys	Arg		
			20					25					30				
Pro	Asn	Pro	Cys	Ala	Tyr	Thr	Pro	Ser	Leu	Lys	Ala	Val	Gln	Arg			
		35					40				45						
Ile	Ala	Glu	Ser	His	Leu	Gln	Ser	Ile	Ser	Asn	Leu	Asn	Glu	Asn	Gln		
	50					55				60							
Ala	Ser	Glu	Glu	Glu	Asp	Glu	Leu	Gly	Glu	Leu	Arg	Glu	Leu	Gly	Tyr		
65				70					75					80			
Pro	Arg	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Asp	Glu	Glu	Glu	Glu		
			85					90					95				
Glu	Glu	Glu	Asp	Ser	Gln	Ala	Glu	Val	Leu	Lys	Val	Ile	Arg	Gln	Ser		
			100					105					110				
Ala	Gly	Gln	Lys	Thr	Thr	Cys	Gly	Gln	Gly	Leu	Glu	Gly	Pro	Trp	Glu		

115 120 125
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
 130 135 140
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
 145 150 155 160
 Pro Ser Pro Ser Glu Pro Gly Thr
 165

<210> 91
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..47

<220>
 <221> CDS
 <222> 48..1301

<220>
 <221> 3'UTR
 <222> 1302..1417

<220>
 <221> polyA_signal
 <222> 1360..1365

<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91
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 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
 1 5 10
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
 15 20 25
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
 30 35 40
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
 45 50 55 60
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 65 70 75
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 80 85 90
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 95 100 105
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 110 115 120

ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac	536
Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His	
125 130 135 140	
tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa	584
Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys	
145 150 155	
cag atc aac gat tac gtg gag aag ggt act caa ggg aaa att gtg gat	632
Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp	
160 165 170	
ttg gtc aag gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac	680
Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr	
175 180 185	
atc ttc ttt aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc	728
Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr	
190 195 200	
gag gaa gag gac ttc cac gtg gac cag gcg acc acc gtg aag gtg cct	776
Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val Lys Val Pro	
205 210 215 220	
atg atg aag cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg	824
Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu	
225 230 235	
tcc agc tgg gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc	872
Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile	
240 245 250	
ttc ttc ctg cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc	920
Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu	
255 260 265	
acc cac gat atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct	968
Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser	
270 275 280	
gcc agc tta cat tta ccc aaa ctg tcc att act gga acc tat gat ctg	1016
Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu	
285 290 295 300	
aag agc gtc ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg	1064
Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly	
305 310 315	
gct gac ctc tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag	1112
Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys	
320 325 330	
gcc gtg cat aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct	1160
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala	
335 340 345	
gct ggg gcc atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag	1208
Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu	
350 355 360	
gtc aag ttc aac aaa ccc ttt gtc ttc tta atg att gaa caa aat acc	1256
Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr	
365 370 375 380	
aag tct ccc ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa	1301
Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys	
385 390 395	
taactgcctc tcgctcctca acccctcccc tccatccctg gccccctccc tggatgacat	1361
taaagaaggg ttgagctggt ccctgcctgc atgtgactgc aaaaaaaaaa aaaaaa	1417

<210> 92

<211> 418

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..24

<400> 92

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Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
-5 1 5
Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
10 15 20
Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
25 30 35 40
Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
45 50 55
Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
60 65 70
His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro
75 80 85
Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
90 95 100
Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
105 110 115 120
Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
125 130 135
Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
140 145 150
Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
155 160 165
Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
170 175 180
Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
185 190 195 200
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val
205 210 215
Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
220 225 230
Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
235 240 245
Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
250 255 260
Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
265 270 275 280
Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
285 290 295
Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
300 305 310
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
315 320 325
Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
330 335 340
Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
345 350 355 360
Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
365 370 375
Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
380 385 390
Gln Lys

<210> 93

<211> 1115

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..277

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 <222> 278..733

<220>
 <221> 3'UTR
 <222> 734..1115

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 <222> 1072..1077

<220>
 <221> polyA_site
 <222> 1101..1115

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 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
 gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
 Met His Phe Gly Leu Leu
 -15
 tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
 Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
 -10 -5 1
 gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
 Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
 5 10 15 20
 aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
 Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
 25 30 35
 aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
 Lys Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg Gln Cys
 40 45 50
 gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
 Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
 55 60 65
 agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
 Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
 70 75 80
 att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
 Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
 85 90 95 100
 gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
 Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
 105 110 115
 aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
 Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
 120 125 130
 gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggg 783
 Ala Ile
 ccgaatgggt tccagggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
 actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaac aatgatggg 903
 tggaagaatg cggtcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963
 atgttctttc taggattgga tagcatttca tgccatgtt aatattttgtg cttttggcat 1023
 ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
 atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94
 <211> 152

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..19

<400> 94
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 -15 -10 -5
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 30 35 40 45
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys
 80 85 90
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr
 95 100 105
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser
 110 115 120 125
 Ser Met Val Asp Ala Trp Ala Ile
 130

<210> 95
 <211> 1307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..252

<220>
 <221> CDS
 <222> 253..744

<220>
 <221> 3'UTR
 <222> 745..1307

<220>
 <221> polyA_signal
 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1292..1307

<400> 95
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 ctctttcact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
 gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala
 -25 -20 -15
 tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339

Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp
 -10 -5 1
 tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca 387
 Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro
 5 10 15
 cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc 435
 Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly
 20 25 30
 cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga 483
 Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Asn Ile Phe Thr Arg
 35 40 45 50
 cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga 531
 Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg
 55 60 65
 ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca 579
 Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala
 70 75 80
 aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc 627
 Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys
 85 90 95
 ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat 675
 Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
 100 105 110
 ttt tat aac aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga 723
 Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
 115 120 125 130
 tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgca agaacatttg 774
 Cys Leu Gly Asn Gln Gln Phe
 135
 tgaagatggg ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa 834
 taactccctg actccgcaat caaccaaggt tcccagcctt tttgaatttc acggtccctc 894
 atggtgtctc actccagcag acagaggatt gtgtcgtgcc aatgagaaca gattctacta 954
 caattcagtc attgggaaat gccgcccatt taagtacagt ggatgtgggg gaaatgaaaa 1014
 caattttact tccaaacaag aatgtctgag ggcattgtaaa aaagggtttca tccaaagaat 1074
 atcaaaagga ggcctaatta aaaccaaag aaaaagaaag aagcagagag tgaaaatagc 1134
 atatgaagaa atttttgtta aaaatatgtg aattttgttat agcaatgtaa cattaattct 1194
 actaaatatt ttatatgaaa tgtttcacta tgattttcta tttttcttct aaaatgcttt 1254
 taattaatat gttcattaata ttttctatgc ttattgcaaa aaaaaaaaaa aaa 1307

<210> 96

<211> 164

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..28

<400> 96

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 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
 40 45 50
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
 55 60 65
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
 70 75 80

Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
85 90 95 100
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
105 110 115
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
120 125 130
Asn Gln Gln Phe
135

<210> 97
<211> 1855
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..504

<220>
<221> 3'UTR
<222> 505..1855

<220>
<221> polyA_signal
<222> 1819..1824

<220>
<221> polyA_site
<222> 1840..1855

<400> 97
tccccggcgcg ccgcccgttgc gctcgccgcg ctgcactga agccccgggcc ctgcgcgcgcc 60
gcgggttcgcc ccgcagcctc gcccctgcc caccggggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100 105
gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
Ala

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cctcccaggc ccctggggca gccctcccgc cgcaggtttc aggtcccagg ccccagctga 614
ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
cgtgttcgcc atcaactgcg ccggcgccag ccacgcccgtc acgcaggcct gttctatggg 734
cgagctgctg cagtgcggct gccaggcgcc ccgcggggcg gccctcccc ggccctccgg 794
cctgcccggc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgcgcctg 854
ggagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914
ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974
cgaggcgggc aggtggccg tgcggagcca cacgcgcacc gagtgc aaat gccacgggct 1034
gtcgggatca tgcgcgctgc gcacctgctg gcagaagctg cctccatttc gcgaggtggg 1094
cgcgcggtg ctggagcgct tccacggcgc ctcacgcgtc atgggcacca acgacggcaa 1154
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cgccgattcg cccgacttct gcgcccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
tcgcgcctgc aatagcagcg ccccggaact cagcggtgctg gacctgctgt gctgcggccg 1334
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ctgctagta cagtccacc gctgccgtgt gcgcaaggag ctcagcctct gcctgtgacc 1454
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gcaccggcac cgggcgcctc tcgcgcgtcg agcccagcct ctccctgcca aagcccaact 1574
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cagggcgcca gacggcccg aaaaggcgt cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct agggagaaac agttttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tcccagaac tgctggccac aggatgggtg gtgaggttag 1814
tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

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<210> 98
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

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<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
      -20      -15      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5      1      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10      15      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25      30      35      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45      50      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60      65      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
      75      80      85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
      90      95      100
Ala
105

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<210> 99
 <211> 667
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..94

<220>
 <221> CDS

<222> 95..613

<220>

<221> 3'UTR

<222> 614..667

<220>

<221> polyA_signal

<222> 636..641

<220>

<221> polyA_site

<222> 652..667

<400> 99

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gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
Met Ile Val Lys Gly Val Ala

1 5
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Gly Asn Trp Leu Phe Ser
10 15 20
tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
25 30 35
gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
40 45 50 55
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
60 65 70
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
75 80 85
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
90 95 100
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
105 110 115
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
120 125 130 135
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
140 145 150
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
155 160 165
caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643
Gln Thr Thr Val Lys Asn
170
tctttcgcaa aaaaaaaaaa aaaa 667

<210> 100

<211> 173

<212> PRT

<213> Homo sapiens

<400> 100

Met Ile Val Lys Gly Val Ala Ser Arg Thr Val Val Ser Arg Pro Phe
1 5 10 15
Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly

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      20      25      30
Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
      35      40      45
Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val
      50      55      60
Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
      65      70      75      80
His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
      85      90      95
Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
      100      105      110
Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
      115      120      125
Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser
      130      135      140
Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
      145      150      155      160
Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
      165      170

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<210> 101
<211> 1062
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..153

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<220>
<221> CDS
<222> 154..639

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<220>
<221> 3'UTR
<222> 640..1062

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<220>
<221> polyA_signal
<222> 1023..1028

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<220>
<221> polyA_site
<222> 1047..1062

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gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc 120
gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
Met Ala Cys Trp Pro Gln Leu
      1      5
agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys
      10      15      20
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
      25      30      35
atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat 318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
      40      45      50      55
ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag 366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
      60      65      70

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ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
75 80 85
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
90 95 100
cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp
105 110 115
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc 558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
120 125 130 135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag 606
Lys Lys Ser Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
140 145 150
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg 659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
155 160
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatac gccagatgg 719
cctgaagtaa ctgaagaatc acaaaagaag tgaaaaggcc ctgcctcgcc ttaactgatg 779
acgttccacc attgtgattt gttcctgccc caccttaact gaggatgataa ccctgtgaat 839
ttccttctcc tggctcagaa gctccccac tgagcacctt gtgacccct gccctgccc 899
accagagaac aacccccttt gactgtaatt ttccattacc ttcccaaatac ctataaaacg 959
gccccacccc tatctccctt tgctgactct cttttcggac tcagcccacc tgcagccagg 1019
tgaaaaaaac agctttattg ctcacacaaa aaaaaaaaaa aaa 1062

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<210> 102
 <211> 162
 <212> PRT
 <213> Homo sapiens

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<400> 102
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1 5 10 15
Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Glu Val Ala Trp Pro
20 25 30
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
35 40 45
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
50 55 60
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
65 70 75 80
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
85 90 95
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
100 105 110
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
115 120 125
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
130 135 140
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
145 150 155 160
Leu Leu

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<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

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 <222> 150..392

<220>
 <221> 3'UTR
 <222> 393..933

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 <222> 63..933

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 ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
 cagatgtgta cggatgaaaa tacagttag atg agt cag aaa ccg gcc aag gag 173
 Met Ser Gln Lys Pro Ala Lys Glu
 1 5
 ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
 Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
 10 15 20
 cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
 His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
 25 30 35 40
 gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
 Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
 45 50 55
 gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
 Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
 60 65 70
 aag atc agg cca acc cca aag aag aag tgaccaagga ggagttttaa 412
 Lys Ile Arg Pro Thr Pro Lys Lys Lys
 75 80
 ytgaatgaac aacctcggt cctggactca ttgcttcaca acccatctac cctgggatga 472
 agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
 gctcatgggc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
 tcatccatt gtcttctgac ctctataatt ggcactgaga gatctgctgt cagtctgctt 652
 atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
 tggaaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
 gcgtgggtggc gggcgctgt ggtcccagct actcgggagg ctgagggcagg agaatggcgt 832
 gaacctggga ggcggagctt gcagttagcc gagatcgac cactgcactc cagcctgggc 892
 gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933

<210> 104
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 104
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 Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
 20 25 30
 Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
 35 40 45
 Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
 50 55 60
 Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
 65 70 75 80
 Lys

<210> 105
 <211> 1187

<212> DNA
<213> Homo sapiens

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<222> 35..1069

<220>
<221> 3'UTR
<222> 1070..1187

<220>
<221> polyA_signal
<222> 1146..1151

<220>
<221> polyA_site
<222> 1172..1187

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Met Ile Ser Pro Val Leu Ile
-15
ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103
Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys
-10 -5 1 5
ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr
10 15 20
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr
25 30 35
gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247
Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu
40 45 50
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala
55 60 65
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro
70 75 80 85
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala
90 95 100
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro
105 110 115
gtc tgt gct ccc atc atc tgc cct cca tcc ata cct acg ttt gca 487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala
120 125 130
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg
135 140 145
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat 583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn
150 155 160 165
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa 631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu
170 175 180

tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt	679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe	
185 190 195	
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca	727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr	
200 205 210	
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa	775
Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu	
215 220 225	
tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct	823
Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser	
230 235 240 245	
tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga	871
Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg	
250 255 260	
gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa	919
Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys	
265 270 275	
gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag	967
Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu	
280 285 290	
gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag	1015
Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys	
295 300 305	
gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag	1063
Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys	
310 315 320 325	
cca tgc taagggtggtt ttcagattcc acataaaatg tcacacttgt ttcttgttca	1119
Pro Cys	
tcceaaggaac ctaattgaaa tttaaaaata aagctactga atttattgcc gcaaaaaaaaa	1179
aaaaaaaa	1187

<210> 106

<211> 345

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<400> 106

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1 5 10	
Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr	
15 20 25	
Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe	
30 35 40 45	
Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr	
50 55 60	
Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg	
65 70 75	
Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr	
80 85 90	
Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly	
95 100 105	
Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro	
110 115 120 125	
Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala	
130 135 140	
Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro	

Asp	Gln	Phe	Leu	Glu	Asp	Val	Arg	Leu	Gln	Glu	Arg	Thr	Ser	Gly	Gly		
				65					70					75			
ttg	ttg	tca	gag	gcc	cca	aat	gaa	aaa	ctc	ttc	ttc	gtg	gac	act	ggc	291	
Leu	Leu	Ser	Glu	Ala	Pro	Asn	Glu	Lys	Leu	Phe	Phe	Val	Asp	Thr	Gly		
			80					85					90				
tcc	aag	gaa	aaa	ggg	ctg	aca	aag	aag	aga	acc	aaa	gtc	cag	aag	aag	339	
Ser	Lys	Glu	Lys	Gly	Leu	Thr	Lys	Lys	Arg	Thr	Lys	Val	Gln	Lys	Lys		
		95					100					105					
tca	ctg	ctt	ctc	aag	aaa	ccc	ctt	cgg	gtt	gac	ctc	atc	ctc	gag	aac	387	
Ser	Leu	Leu	Leu	Lys	Lys	Pro	Leu	Arg	Val	Asp	Leu	Ile	Leu	Glu	Asn		
		110					115					120					
aca	tcc	aaa	gtc	cct	gcc	ccc	aaa	gac	gtc	ctc	gcc	cac	cag	gtc	ccc	435	
Thr	Ser	Lys	Val	Pro	Ala	Pro	Lys	Asp	Val	Leu	Ala	His	Gln	Val	Pro		
					125		130			135					140		
aac	gcc	aag	aag	ctc	agg	cgg	aag	gag	cag	cta	tgg	gag	aag	ctg	gcc	483	
Asn	Ala	Lys	Lys	Leu	Arg	Arg	Lys	Glu	Gln	Leu	Trp	Glu	Lys	Leu	Ala		
				145					150				155				
aag	cag	ggc	gag	ctg	ccc	cgg	gag	gtg	cgc	agg	gcc	cag	gcc	cgg	ctc	531	
Lys	Gln	Gly	Glu	Leu	Pro	Arg	Glu	Val	Arg	Arg	Ala	Gln	Ala	Arg	Leu		
			160					165					170				
ctc	aac	cct	tct	gca	aca	agg	gcc	aag	ccc	ggg	ccc	cag	gac	acc	gta	579	
Leu	Asn	Pro	Ser	Ala	Thr	Arg	Ala	Lys	Pro	Gly	Pro	Gln	Asp	Thr	Val		
			175				180					185					
gag	cgg	ccc	ttc	tac	gac	ctc	tgg	gcc	tca	gac	aac	ccc	ctg	gac	agg	627	
Glu	Arg	Pro	Phe	Tyr	Asp	Leu	Trp	Ala	Ser	Asp	Asn	Pro	Leu	Asp	Arg		
		190				195					200						
ccg	ttg	gtt	ggc	cag	gat	gag	ttt	ttc	ctg	gag	cag	acc	aag	aag	aaa	675	
Pro	Leu	Val	Gly	Gln	Asp	Glu	Phe	Phe	Leu	Glu	Gln	Thr	Lys	Lys	Lys		
					205		210			215			220				
gga	gtg	aag	cgg	cca	gca	cgc	ctg	cac	acc	aag	cgg	tcc	cag	gca	ccc	723	
Gly	Val	Lys	Arg	Pro	Ala	Arg	Leu	His	Thr	Lys	Pro	Ser	Gln	Ala	Pro		
				225				230					235				
gcc	gtg	gag	gtg	gcg	cct	gcc	gga	gct	tcc	tac	aat	cca	tcc	ttt	gaa	771	
Ala	Val	Glu	Val	Ala	Pro	Ala	Gly	Ala	Ser	Tyr	Asn	Pro	Ser	Phe	Glu		
			240				245					250					
gac	cac	cag	acc	ctg	ctc	tca	gcg	gcc	cac	gag	gtg	gag	ttg	cag	cgg	819	
Asp	His	Gln	Thr	Leu	Leu	Ser	Ala	Ala	His	Glu	Val	Glu	Leu	Gln	Arg		
		255				260						265					
cag	aag	gag	gcg	gag	aag	ctg	gag	cgg	cag	ctg	gcc	ctg	ccc	gcc	acg	867	
Gln	Lys	Glu	Ala	Glu	Lys	Leu	Glu	Arg	Gln	Leu	Ala	Leu	Pro	Ala	Thr		
		270				275					280						
gag	cag	gcc	gcc	acc	cag	gag	tcc	aca	ttc	cag	gag	ctg	tgc	gag	ggg	915	
Glu	Gln	Ala	Ala	Thr	Gln	Glu	Ser	Thr	Phe	Gln	Glu	Leu	Cys	Glu	Gly		
				285		290				295					300		
ctg	ctg	gag	gag	tcg	gat	ggg	gag	ggg	gag	cca	ggc	cag	ggc	gag	ggg	963	
Leu	Leu	Glu	Glu	Ser	Asp	Gly	Glu	Gly	Glu	Pro	Gly	Gln	Gly	Glu	Gly		
				305				310					315				
ccg	gag	gct	ggg	gat	gcc	gag	gtc	tgt	ccc	acg	ccc	gcc	cgc	ctg	gcc	1011	
Pro	Glu	Ala	Gly	Asp	Ala	Glu	Val	Cys	Pro	Thr	Pro	Ala	Arg	Leu	Ala		
		320						325				330					
acc	aca	gag	aag	aag	acg	gag	cag	cag	cgg	cgg	cgg	gag	aag	gct	gtg	1059	
Thr	Thr	Glu	Lys	Lys	Thr	Glu	Gln	Gln	Arg	Arg	Arg	Glu	Lys	Ala	Val		
		335				340						345					
cac	agg	ctg	cgg	gta	cag	cag	gcc	gcg	ttg	cgg	gcc	gcc	cgg	ctc	cgg	1107	
His	Arg	Leu	Arg	Val	Gln	Gln	Ala	Ala	Leu	Arg	Ala	Ala	Arg	Leu	Arg		
		350				355					360						
cac	cag	gag	ctg	ttc	cgg	ctg	cgc	ggg	atc	aag	gcc	cag	gtg	gcc	ctg	1155	
His	Gln	Glu	Leu	Phe	Arg	Leu	Arg	Gly	Ile	Lys	Ala	Gln	Val	Ala	Leu		
		365			370			375						380			
agg	ctg	gcg	gag	ctg	gcg	cgg	cgg	cag	agg	cgg	cgg	cag	gcg	cgg	cgg	1203	
Arg	Leu	Ala	Glu	Leu	Ala	Arg	Arg	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Arg		
				385				390					395				
gag	gct	gag	gct	gac	aag	ccc	cga	agg	ctg	ggg	cgg	ctc	aag	tac	cag	1251	

Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln	
400 405 410	
gca cct gac atc gac gtg cag ctg agc tcg gag ctg aca gac tcg ctc	1299
Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu	
415 420 425	
agg acc ctg aag ccc gag ggc aac atc ctt cga gac cgg ttc aag agc	1347
Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser	
430 435 440	
ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa	1395
Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys	
445 450 455 460	
cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc	1443
Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile	
465 470 475	
cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaa aatctcttct	1499
Gln Leu	
agctcaaaaa aaaaaaaaaa a	1520

<210> 108

<211> 478

<212> PRT

<213> Homo sapiens

<400> 108

Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser	
1 5 10 15	
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Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp	
35 40 45	
Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu	
50 55 60	
Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu	
65 70 75 80	
Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys	
85 90 95	
Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu	
100 105 110	
Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val	
115 120 125	
Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys	
130 135 140	
Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu	
145 150 155 160	
Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser	
165 170 175	
Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe	
180 185 190	
Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly	
195 200 205	
Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg	
210 215 220	
Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val	
225 230 235 240	
Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr	
245 250 255	
Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala	
260 265 270	
Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala	
275 280 285	
Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu	
290 295 300	
Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly	

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305          310          315          320
Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys
          325          330          335
Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg
          340          345          350
Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu
          355          360          365
Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu
          370          375          380
Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala
385          390          395          400
Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile
          405          410          415
Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys
          420          425          430
Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg
          435          440          445
Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys
          450          455          460
Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
465          470          475

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<210> 109
<211> 1789
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..94

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<220>
<221> CDS
<222> 95..1252

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<220>
<221> 3'UTR
<222> 1253..1789

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<220>
<221> polyA_signal
<222> 1751..1756

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<220>
<221> polyA_site
<222> 1774..1789

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ggctcttgcaa tatttattct gctttcgggt agatgggagg cccgggggacc tggctggggt 60
tctgccaagc ttctccgata cccaggtttc ataa atg tgt ttg ttg ctt tcc tgc 115
Met Cys Leu Leu Leu Ser Cys
-10
cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163
Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr
-5 1 5
tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211
Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu
10 15 20 25
gtg gtg cac atg tcg cag acc aca att agt cct ctg gag aat gcc ata 259
Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile
30 35 40
gaa acc atg tcc acg gcc aat gag aag atc ctg atg atg ata aac cag 307
Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln

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	45	50	55	
tac cag agt gat gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg				355
Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu				
	60	65	70	
aac ggg att gtg gac cct gct gtc atg gga ggc ttc gcc aag tat gag				403
Asn Gly Ile Val Asp Pro Ala Val Met Gly Gly Phe Ala Lys Tyr Glu				
	75	80	85	
aag gcc ttc ttc act gaa gag tat gtc agg gac cac cct gag gac cag				451
Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg Asp His Pro Glu Asp Gln				
	90	95	100	105
gac aag ctg acc cac ctc aag gac ctg att gca tgg cag atc ccc ttc				499
Asp Lys Leu Thr His Leu Lys Asp Leu Ile Ala Trp Gln Ile Pro Phe				
	110	115	120	
ttg gga gct ggg att aag atc cat gag aaa agg gtg tca gat aac ttg				547
Leu Gly Ala Gly Ile Lys Ile His Glu Lys Arg Val Ser Asp Asn Leu				
	125	130	135	
cga ccc ttc cat gac cgg atg gag gaa tgt ttc aag aac ctg aaa atg				595
Arg Pro Phe His Asp Arg Met Glu Glu Cys Phe Lys Asn Leu Lys Met				
	140	145	150	
aag gtg gag aag gag tac ggt gtc cga gag atg cct gac ttt gac gac				643
Lys Val Glu Lys Glu Tyr Gly Val Arg Glu Met Pro Asp Phe Asp Asp				
	155	160	165	
agg aga gtg ggc cgt ccc agg tct atg ctg cgc tca tac aga cag atg				691
Arg Arg Val Gly Arg Pro Arg Ser Met Leu Arg Ser Tyr Arg Gln Met				
	170	175	180	185
tcc atc atc tct ctg gct tcc atg aat tct gac tgc agc acc ccc agc				739
Ser Ile Ile Ser Leu Ala Ser Met Asn Ser Asp Cys Ser Thr Pro Ser				
	190	195	200	
aag cct acc tca gag agc ttt gac ctg gaa tta gca tca ccc aag acg				787
Lys Pro Thr Ser Glu Ser Phe Asp Leu Glu Leu Ala Ser Pro Lys Thr				
	205	210	215	
ccg aga gtg gag cag gag gaa ccg atc tcc ccg ggg agc acc ctg cct				835
Pro Arg Val Glu Gln Glu Glu Pro Ile Ser Pro Gly Ser Thr Leu Pro				
	220	225	230	
gag gtc aag ctg cgg agg tcc aag aag agg aca aag aga agc agc gta				883
Glu Val Lys Leu Arg Arg Ser Lys Lys Arg Thr Lys Arg Ser Ser Val				
	235	240	245	
gtt ttt gcg gat gag aaa gca gct gca gag tcg gac ctg aag cgg ctt				931
Val Phe Ala Asp Glu Lys Ala Ala Ala Glu Ser Asp Leu Lys Arg Leu				
	250	255	260	265
tcc agg aag cat gag ttc atg agt gac acc aac ctc tcg gag cat gcg				979
Ser Arg Lys His Glu Phe Met Ser Asp Thr Asn Leu Ser Glu His Ala				
	270	275	280	
gcc atc ccc ctc aag gcg tct gtc ctc tct caa atg agc ttt gcc agc				1027
Ala Ile Pro Leu Lys Ala Ser Val Leu Ser Gln Met Ser Phe Ala Ser				
	285	290	295	
cag tcc atg cct acc atc cca gcc ctg gcg ctc tca gtg gca ggc atc				1075
Gln Ser Met Pro Thr Ile Pro Ala Leu Ala Leu Ser Val Ala Gly Ile				
	300	305	310	
cct ggg ttg gat gag gcc aac aca tct ccc cgc ctc agc cag acc ttc				1123
Pro Gly Leu Asp Glu Ala Asn Thr Ser Pro Arg Leu Ser Gln Thr Phe				
	315	320	325	
ctc caa ctc tca gat ggt gac aag aag aca ctc aca cgg aag aag gtc				1171
Leu Gln Leu Ser Asp Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val				
	330	335	340	345
aat cag ttc ttc aag aca atg ctg gcc agc aaa tcg gct gaa gaa ggc				1219
Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly				
	350	355	360	
aaa cag atc cca gac tcg ctg tcc acg gac ctg tgagctgctg ctgactaggg				1272
Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu				
	365	370		
ctgcatggga gagccagggga ggggagtttc tggaagagga aagccatgcg tggaacatcg				1332
aagcctcaga gagtgggaga ctgtcccat cagttgtcct tacttagagg agacagagag				1392

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gccaatcagg tcccagagct tgaatgctaa caagcccagc atccccctggg gctgtgatca 1452
tggtggatga ggaagcctca acgtagattc ctgaactcaa ggtaccagca agaatgcctt 1512
ctcccagtggt gctctcccca acatcctagg cacagctttc ataaccaggt ttcttaggtg 1572
taagaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt 1632
taaataattct ttttaatttt attttagatt aacagttttg tactttacat tttttatac 1692
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<210> 110
<211> 386
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..15

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Ser Met Trp Ile Glu Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro
5 10 15
Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
20 25 30
Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
35 40 45
Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
50 55 60 65
Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
70 75 80
Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
85 90 95
Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
100 105 110
Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
115 120 125
Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
130 135 140 145
Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
150 155 160
Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
165 170 175
Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
180 185 190
Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
195 200 205
Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
210 215 220 225
Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
230 235 240
Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
245 250 255
Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
260 265 270
Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
275 280 285
Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
290 295 300 305
Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
310 315 320
Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
325 330 335
Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala

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tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
 150 155 160
 atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt 642
 Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu
 165 170 175 180
 ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act 690
 Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr
 185 190 195
 gtg gag gtc aca aag acg ttt ttg cct ctt aga aaa tcc aaa ggg 738
 Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly
 200 205 210
 agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg 786
 Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg
 215 220 225
 ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca 834
 Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser
 230 235 240
 gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc 882
 Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile
 245 250 255 260
 caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg 930
 Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp
 265 270 275
 gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag 978
 Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln
 280 285 290
 gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta 1026
 Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu
 295 300 305
 ttg atc aac tcg tta gcc agc aag gac ttc tct ccg gtg ctg cgg gac 1074
 Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp
 310 315 320
 atc cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac acg cca 1122
 Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro
 325 330 335 340
 ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att 1170
 Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile
 345 350 355
 ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc 1218
 Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro
 360 365 370
 atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc 1263
 Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro
 375 380 385
 taggcaatgg aagccctcaa agaagtcgga atgtcatagt cttgaaatga aagggaaact 1323
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<210> 112

<211> 387

<212> PRT

<213> Homo sapiens

<400> 112

Met Ser Thr Phe Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro
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 Thr Val Leu Cys Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly
 20 25 30
 Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys
 35 40 45
 Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser
 50 55 60

Cys	Phe	Leu	Met	Tyr	Thr	Tyr	Leu	Ser	Gly	Gln	Glu	Leu	Leu	Pro	Val	65	70	75	80
Asp	Gln	Lys	Ala	Val	Leu	Val	Thr	Gly	Gly	Asp	Cys	Gly	Leu	Gly	His	85	90	95	
Ala	Leu	Cys	Lys	Tyr	Leu	Asp	Glu	Leu	Gly	Phe	Thr	Val	Phe	Ala	Gly	100	105	110	
Val	Leu	Asn	Glu	Asn	Gly	Pro	Gly	Ala	Glu	Glu	Leu	Arg	Arg	Thr	Cys	115	120	125	
Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln	130	135	140	
Ile	Lys	Asp	Ala	Tyr	Ser	Lys	Val	Ala	Ala	Met	Leu	Gln	Asp	Arg	Gly	145	150	155	160
Leu	Trp	Ala	Val	Ile	Asn	Asn	Ala	Gly	Val	Leu	Gly	Phe	Pro	Thr	Asp	165	170	175	
Gly	Glu	Leu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn	180	185	190	
Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg	195	200	205	
Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala	210	215	220	
Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr	225	230	235	240
Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys	245	250	255	
Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr	260	265	270	
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro	275	280	285	
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg	290	295	300	
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro	305	310	315	320
Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala	325	330	335	
Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His	340	345	350	
Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly	355	360	365	
Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys	370	375	380	
Lys	Ala	Pro														385			